

## APPENDIX A

**results of BLAST****BLASTP 2.2.5 [Nov-16-2002]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1048867675-017493-20634

**Query=**

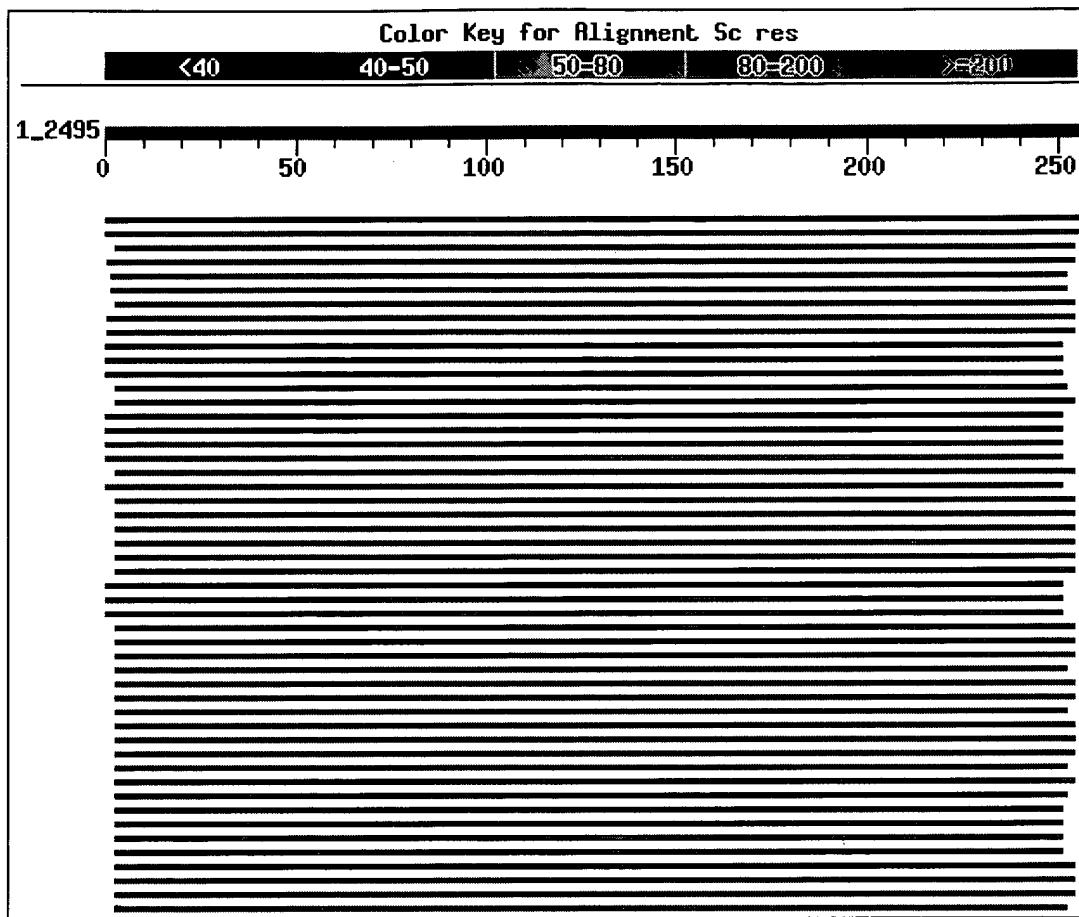
(256 letters)

**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF  
1,384,147 sequences; 445,599,717 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



#### Related Structures

		Score (bits)	E Value
Sequences producing significant alignments:			
gi 15924001 ref NP_371535.1	trans-2-enoyl-ACP reductase [S...	458	e-128
gi 27467630 ref NP_764267.1	trans-2-enoyl-ACP reductase [S...	424	e-118
gi 21399142 ref NP_655127.1	adh_short, short chain dehydro...	300	1e-80
gi 15615406 ref NP_243709.1	enoyl-[acyl-carrier protein] r...	282	3e-75
gi 7531269 sp P54616 FABI_BACSU	Enoyl-[acyl-carrier-protein...]	281	6e-75
gi 16078237 ref NP_389054.1	similar to enoyl- acyl-carrier...	280	1e-74
gi 23097678 ref NP_691144.1	enoyl-[acyl-carrier protein] r...	248	6e-65
gi 16800038 ref NP_470306.1	similar to enoyl- acyl-carrier...	244	7e-64
gi 16803010 ref NP_464495.1	similar to enoyl- acyl-carrier...	244	9e-64
gi 15420715 gb AAK97428.1 AF382392_4	enoyl carrier reductas...	239	3e-62
gi 23128764 gb ZP_00110603.1	hypothetical protein [Nostoc ...	236	3e-61
gi 13924473 gb AAK49021.1 AF195898_2	enoyl-[acyl-carrier-pr...	234	1e-60
gi 23019970 ref ZP_00059677.1	hypothetical protein [Clostr...	234	1e-60
gi 23475798 ref ZP_00131074.1	hypothetical protein [Desulf...	233	3e-60
gi 6686259 sp Q05069 FABI_ANASP	Enoyl-[acyl-carrier-protein...	232	5e-60
gi 17231883 ref NP_488431.1	enoyl-[acyl-carrier-protein] r...	232	5e-60
gi 23122150 gb ZP_00104285.1	hypothetical protein [Prochlo...	224	7e-58
gi 23132326 gb ZP_00114111.1	hypothetical protein [Prochlo...	224	9e-58
gi 23110472 gb ZP_00096626.1	hypothetical protein [Novosph...	224	1e-57
gi 22299236 ref NP_682483.1	enoyl-[acyl-carrier-protein] r...	221	1e-56
gi 15964651 ref NP_385004.1	PUTATIVE ENOYL-ACYL-CARRIER-PR...	219	4e-56
gi 22958522 gb ZP_0006191.1	hypothetical protein [Rhodoba...	218	5e-56
gi 22963177 gb ZP_00010783.1	hypothetical protein [Rhodops...	218	6e-56

gi 15888100 ref NP_353781.1	AGR_C_1374p [Agrobacterium tum... 217	1e-55
gi 17987795 ref NP_540429.1	ENOYL-(ACYL-CARRIER-PROTEIN) R... 216	3e-55
gi 13476200 ref NP_107770.1	enoyl-acyl carrier protein red... 216	4e-55
gi 23132906 ref ZP_00114680.1	hypothetical protein [Synech... 214	7e-55
gi 16329628 ref NP_440356.1	enoyl-[acyl-carrier-protein] r... 214	1e-54
gi 6685443 sp P73016 FABI_SINY3	Enoyl-[acyl-carrier-protein... 214	1e-54
gi 22966064 gb ZP_00013661.1	hypothetical protein [Rhodosp... 213	2e-54
gi 23055279 gb ZP_00081394.1	hypothetical protein [Geobact... 210	2e-53
gi 27377740 ref NP_769269.1	NADH-enoyl acyl carrier protei... 210	2e-53
gi 23059616 ref ZP_00084568.1	hypothetical protein [Pseudo... 209	4e-53
gi 23015709 gb ZP_00055478.1	hypothetical protein [Magneto... 208	7e-53
gi 22970115 gb ZP_00017264.1	hypothetical protein [Chlorof... 207	8e-53
gi 23103009 gb ZP_00089502.1	hypothetical protein [Azotoba... 207	1e-52
gi 15602047 ref NP_245119.1	Fabi [Pasteurella multocida] >... 206	3e-52
gi 13474637 ref NP_106206.1	enoyl-[acyl-carrier-protein] r... 204	9e-52
gi 17988241 ref NP_540875.1	ENOYL-(ACYL-CARRIER-PROTEIN) R... 204	1e-51
gi 15792718 ref NP_282541.1	putative enoyl-[acyl-carrier-p... 203	2e-51
gi 15611251 ref NP_222902.1	ENOYL-ACYL CARRIER PROTEIN RED... 203	2e-51
gi 17545891 ref NP_519293.1	PROBABLE ENOYL-[ACYL-CARRIER-P... 203	2e-51
gi 26247623 ref NP_753663.1	Enoyl-[acyl-carrier-protein] r... 202	4e-51
gi 15801888 ref NP_287908.1	enoyl-[acyl-carrier-protein] r... 202	5e-51
gi 2914323 pdb 1DFG A	Chain A, X-Ray Structure Of Escherich... 202	5e-51
gi 5822339 pdb 1QSG A	Chain A, Crystal Structure Of Enoyl R... 202	5e-51
gi 15672548 ref NP_266722.1	NADH-dependent enoyl-ACP reduc... 201	7e-51
gi 27375882 ref NP_767411.1	NADH-enoyl acyl carrier protei... 201	7e-51
gi 22975990 gb ZP_00021907.1	hypothetical protein [Ralston... 201	7e-51
gi 22982236 ref ZP_00027522.1	hypothetical protein [Burkho... 201	7e-51
gi 6688578 emb CAB65183.1	enoyl reductase [Legionella pneu... 201	8e-51
gi 23469163 ref ZP_00124498.1	hypothetical protein [Pseudo... 200	2e-50
gi 15892417 ref NP_360131.1	putative enoyl-[acyl carrier p... 200	2e-50
gi 22962420 gb ZP_00010026.1	hypothetical protein [Rhodops... 199	2e-50
gi 15604232 ref NP_220748.1	PUTATIVE ENOYL-[ACYL-CARRIER-P... 199	2e-50
gi 28261966 gb EAA25470.1	putative enoyl-[acyl carrier pro... 199	4e-50
gi 28378371 ref NP_785263.1	enoyl-[acyl-carrier protein] r... 198	6e-50
gi 28870876 ref NP_793495.1	enoyl-(acyl-carrier-protein) r... 198	7e-50
gi 16760180 ref NP_455797.1	enoyl-[acyl-carrier-protein] r... 198	8e-50
gi 16765044 ref NP_460659.1	enoyl-[acyl-carrier-protein] r... 197	1e-49
gi 15676251 ref NP_273385.1	enoyl-(acyl-carrier-protein) r... 196	3e-49
gi 23467752 gb ZP_00123331.1	hypothetical protein [Haemoph... 196	3e-49
gi 22955997 gb ZP_00003798.1	hypothetical protein [Nitroso... 195	5e-49
gi 15795023 ref NP_284845.1	enoyl-ACP reductase [Neisseria... 195	5e-49
gi 23000544 gb ZP_00044472.1	hypothetical protein [Magneto... 195	5e-49
gi 16273618 ref NP_439876.1	enoyl-(acyl-carrier-protein) r... 194	1e-48
gi 16127947 ref NP_422511.1	enoyl-(acyl-carrier-protein) r... 194	1e-48
gi 1169593 sp P44432 FABI_HAEIN	Enoyl-[acyl-carrier-protein... 194	1e-48
gi 15644824 ref NP_206994.1	enoyl-(acyl-carrier-protein) r... 192	4e-48
gi 23015759 gb ZP_00055527.1	hypothetical protein [Magneto... 191	1e-47
gi 15597003 ref NP_250497.1	NADH-dependent enoyl-ACP reduc... 189	3e-47
gi 15963999 ref NP_384352.1	PUTATIVE ENOYL-ACYL-CARRIER-PR... 186	3e-46
gi 23103934 gb ZP_00090406.1	hypothetical protein [Azotoba... 184	1e-45
gi 27378570 ref NP_770099.1	NADH-enoyl acyl carrier protei... 183	2e-45
gi 22961734 gb ZP_00009340.1	hypothetical protein [Rhodops... 182	3e-45
gi 7531116 sp O67505 FABI_AQUAE	Enoyl-[acyl-carrier-protein... 182	6e-45
gi 15606690 ref NP_214070.1	enoyl-[acyl-carrier-protein] r... 182	6e-45
gi 15806965 ref NP_295690.1	enoyl-acyl carrier protein red... 181	1e-44
gi 24324009 ref NP_715373.1	Enoyl-[acyl-carrier-protein] r... 179	4e-44
gi 22978855 gb ZP_00024594.1	hypothetical protein [Ralston... 178	5e-44
gi 22983971 ref ZP_00029134.1	hypothetical protein [Burkho... 177	1e-43
gi 15887503 ref NP_353184.1	AGR_C_242p [Agrobacterium tume... 173	2e-42

<u>gi 17934067 ref NP_530857.1 </u>	enoyl-(acyl-carrier-protein) r...	<u>172</u>	<u>3e-42</u>
<u>gi 22960318 gb ZP_00007959.1 </u>	hypothetical protein [Rhodoba...	<u>172</u>	<u>3e-42</u>
<u>gi 22958079 gb ZP_00005759.1 </u>	hypothetical protein [Rhodoba...	<u>172</u>	<u>3e-42</u>
<u>gi 22989400 ref ZP_00034455.1 </u>	hypothetical protein [Burkho...	<u>172</u>	<u>4e-42</u>
<u>gi 21672535 ref NP_660602.1 </u>	enoyl-[acyl-carrier-protein] r...	<u>171</u>	<u>8e-42</u>
<u>gi 22967294 gb ZP_00014888.1 </u>	hypothetical protein [Rhodosp...	<u>170</u>	<u>2e-41</u>
<u>gi 27904742 ref NP_777868.1 </u>	enoyl-[acyl-carrier-protein] r...	<u>169</u>	<u>3e-41</u>
<u>gi 23010640 gb ZP_00051260.1 </u>	hypothetical protein [Magneto...	<u>163</u>	<u>2e-39</u>
<u>gi 15616876 ref NP_240089.1 </u>	enoyl-[acyl-carrier-protein] r...	<u>161</u>	<u>1e-38</u>
<u>gi 21220304 ref NP_626083.1 </u>	putative enoyl-(acyl-carrier-p...	<u>157</u>	<u>1e-37</u>
<u>gi 23004903 gb ZP_00047997.1 </u>	hypothetical protein [Magneto...	<u>145</u>	<u>4e-34</u>
<u>gi 23019834 gb ZP_00059543.1 </u>	hypothetical protein [Thermob...	<u>138</u>	<u>8e-32</u>
<u>gi 15618321 ref NP_224606.1 </u>	Enoyl-Acyl-Carrier Protein Red...	<u>120</u>	<u>2e-26</u>
<u>gi 14422257 emb CAC41367.1 </u>	enoyl-[acyl-carrier protein] re...	<u>117</u>	<u>2e-25</u>
<u>gi 99805 pir  S17761</u>	enoyl-[acyl-carrier-protein] reductase...	<u>117</u>	<u>2e-25</u>
<u>gi 7141083 gb AAF37208.1 AF207593_1</u>	enoyl-ACP reductase [Ar...	<u>117</u>	<u>2e-25</u>
<u>gi 15834999 ref NP_296758.1 </u>	enoyl-(acyl-carrier protein) r...	<u>117</u>	<u>2e-25</u>
<u>gi 18396215 ref NP_565331.1 </u>	enoyl-ACP reductase (enr-A); p...	<u>116</u>	<u>3e-25</u>

## Alignments

~ 103

...>gi|15924001|ref|NP\_371535.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus Mu50]  
gi|15926599|ref|NP\_374132.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus s N315]  
gi|21282621|ref|NP\_645709.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus s MW2]  
gi|25283453|pir||C89869 trans-2-enoyl-ACP reductase [imported] - Staphylococcus a (strain N315)  
gi|6180191|gb|AAF05840.1|AF197058\_1 trans-2-enoyl-ACP reductase [Staphylococcus a  
gi|13700814|dbj|BAB42110.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su N315]  
gi|14246781|dbj|BAB57173.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su Mu50]  
gi|21204059|dbj|BAB94757.1| trans-2-enoyl-ACP reductase [Staphylococcus aureus su MW2]  
Length = 256

Score = 458 bits (1179), Expect = e-128  
 Identities = 242/256 (94%), Positives = 242/256 (94%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNLENKTYVIMGIANKRSIAFGVAKVLQLGAKLVFTY QLNQPEA

Sbjct: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLQLGAKLVFTYRKERSRKELEKLLQLNQPEA 60

Query: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120  
 HLYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI

Sbjct: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120

Query: 121 SSYSLTIVAHHEAKKLMP EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180  
 SSYSLTIVAHHEAKKLMP EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP

Sbjct: 121 SSYSLTIVAHHEAKKLMP EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180

Query: 181 DNIRVNAISA~~G~~PIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSG 240

DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSG  
 Sbjct: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSG 240

Query: 241 VTGENIHVDMSGFHAIK 256  
 VTGENIHVDMSGFHAIK  
 Sbjct: 241 VTGENIHVDMSGFHAIK 256

[>gi|27467630|ref|NP\_764267.1| trans-2-enoyl-ACP reductase [Staphylococcus epidermidis]  
 gi|27315174|gb|AAO04309.1|AE016746\_99 trans-2-enoyl-ACP reductase [Staphylococcus epidermidis]  
 Length = 256

Score = 424 bits (1090), Expect = e-118  
 Identities = 225/256 (87%), Positives = 233/256 (91%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNLENKTYVIMGIANKRSIAFGVAKVLD+LGAKLVFTY QLNQ E  
 Sbjct: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDRLGAKLVFTYRKERSRKELEKLLQLNQSEH 60

Query: 61 HLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDI 120  
 HLY+IDVQ+DE++INGF QIGKDVG IDGVYHSIAFANMEDLRGRFSETSREGFLLAQ+I  
 Sbjct: 61 HLYEIDVQNDEDIINGFSQIGKDVGQIDGVYHSIAFANMEDLRGRFSETSREGFLLAQEI 120

Query: 121 SSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 180  
 SSYSLT+VAHEAKKLMPEGGSIVATTY+GGE AVQNYNVMGVAKASLEANVKYLALDLG  
 Sbjct: 121 SSYSLTLVAHEAKKLMPEGGSIVATTYIGGEAAVQNYNVMGVAKASLEANVKYLALDLGE 180

Query: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSG 240  
 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIE RAPLKRNVQEVGKTAAYLLSDLSSG  
 Sbjct: 181 DNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSG 240

Query: 241 VTGENIHVDMSGFHAIK 256  
 VTGENIHVD GFHAIK  
 Sbjct: 241 VTGENIHVDGGFHAIK 256

[>gi|21399142|ref|NP\_655127.1| adh\_short, short chain dehydrogenase [Bacillus antreibachii]  
 Length = 256

Score = 300 bits (768), Expect = 1e-80  
 Identities = 157/252 (62%), Positives = 191/252 (75%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L+ KT+V+MG+AN+RSIA+G+A+ L GAKL+FTY L E+ +  
 Sbjct: 4 LQGKTFVVMGVANQRSIAWGIARSLHNAGAKLIFTYAGERLERNVRELADTLEGQESLVL 63

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 DV +DEE+ FE I ++VG I GV H IAFAN +DL+G F +TSR+GFLLAQ+IS++  
 Sbjct: 64 PCDVTNDEELTACFETIKQEVTIHGVAHCIAFANRDDLKGEFVDTSRDGFLAQNISAF 123

Query: 124 SLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP 183  
 SLT VA EAKK+M EGG+I+ TYLGGE V+NYNVMGVAKASLEA+VKYLA DLG I  
 Sbjct: 124 SLTAVAREAKKVMTEGGNILTLYLGGERVVKNYNVMGVAKASLEASVKYLANDLGQHGI 183

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGPIRTLSAKGVG FN+IL+EIERAPL+R Q EVG TA +L SDL+ GVTG  
 Sbjct: 184 RVNAISAGPIRTLSAKGVGDFNSILREIEERAPLRRRTTQEEVGDTAVFLSDLARGVTG 243

Query: 244 ENIHDVDSGFHAI 255  
 ENIHDVDSG+H +  
 Sbjct: 244 ENIHDVDSGYHIL 255

[>gi|15615406|ref|NP\_243709.1| enoyl-[acyl-carrier protein] reductase [Bacillus halodurans (strain C-125)]  
 gi|25283450|pir||C84005 enoyl-[acyl-carrier protein] reductase BH2843 [imported]  
 gi|10175464|dbj|BAB06562.1| enoyl-[acyl-carrier protein] reductase [Bacillus halodurans (strain C-125)]  
 Length = 260

Score = 282 bits (722), Expect = 3e-75  
 Identities = 149/254 (58%), Positives = 188/254 (74%)

Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLQDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAH 61  
 L+L ++TYV+MG+ANCRSIA+G+A+ L GA+L+FTY L + +  
 Sbjct: 4 LSLVDRTYVVMGVANKRSIAWGLAQLIFTYAGERLEKNVRLVETLERDDHL 63

Query: 62 LYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDIS 121  
 + + DV SDE V F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +IS  
 Sbjct: 64 VLECDVTSDEAVEATFASIKEQVGTIHGLAHCIAFANKEELEGEYLNTRDGFLAHNIS 123

Query: 122 SYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181  
 +YSLT VA A+ LM EGGSIV TYLGGE V+NVMGVAKASL+A+VKYLA DLG +  
 Sbjct: 124 AYSLTAVAKAARPLMNEGGGSIVTLTYLGGEKVVNRNYNVMGVAKASLDASVKYLANDLGKE 183

Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGV 241  
 NIRVNAISAGPIRTL+AKG+GGFN +L+EIEERAPL+R Q EVG TA +L+SDLS G+  
 Sbjct: 184 NIRVNAISAGPIRTLAKGIGGFNDVLREIEERAPLRRTTQEEVGDTALFLMSDLRSGI 243

Query: 242 TGENIHDVDSGFHAI 255  
 TGE +HVDSG++ +  
 Sbjct: 244 TGEILHVDSGYNIL 257

[>gi|7531269|sp|P54616|FABI\_BACSU Enoyl-[acyl-carrier-protein] reductase [NADH-ubiquinone oxidoreductase (Cold-shock induced protein 15) (CSI15) (Vegetative protein 241) (VEG241)]  
 Length = 258

Score = 281 bits (719), Expect = 6e-75  
 Identities = 144/251 (57%), Positives = 183/251 (72%)

Query: 3 NLENKTYVIMGIANKRSIAFGVAKVLQDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHL 62  
 +LE + V+MG+ANCRSIA+G+A+ L + GA+L+FTY L++ ++ +  
 Sbjct: 4 SLEGRNIVVMGVANKRSIAWGLAQLIFTYAGERLEKSVHEAGLTLDRNDSII 63

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122  
 DV +D E+ F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +ISS  
 Sbjct: 64 LPCDVTNDAEITCFASIKEQVGVVIHGIAHCIAFANKEELVGEYLNTRDGFLAHNIS 123

Query: 123 YSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YSLT V A+ +M EGGSIV TYLGGE + NVMGVAKASL+A+VKYLA DLG +N  
 YSLTAVVKAARPLMNEGGGSIVTLTYLGGEKVVNRNYNVMGVAKASLDASVKYLAADLGKEN 183

3 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGV 242

IRVN+ISAGPIRTLSAKG+ FN+ILK+IEERAPL+R EVG TAA+L SD+S G+T  
 Sbjct: 184 IRVNSISAGPIRTLSAKGISDFNSILKDIEERAPLRTTPEEVGDTAAFLFSDMSRGIT 243

Query: 243 GENIHVDSGFH 253  
 GEN+HVDSGFH  
 Sbjct: 244 GENLHVDSGFH 254

[>gi|16078237|ref|NP\_389054.1| similar to enoyl- acyl-carrier protein reductase [Bacillus subtilis]  
 gi|7431092|pir|G69845 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9  
 Bacillus subtilis)  
 gi|2633526|emb|CAB13029.1| similar to enoyl- acyl-carrier protein reductase [Bacillus subtilis]  
 Length = 269

Score = 280 bits (717), Expect = 1e-74  
 Identities = 144/251 (57%), Positives = 183/251 (72%)

Query: 3 NLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHL 62  
 +LE + V+MG+ANKRSIA+G+A+ L + GA+L+FTY L++ ++ +  
 Sbjct: 15 SLEGRNIVVMGVANKRSIAWGIARSLHEAGARLIFTYAGERLEKSVHELAGTLDRNDSII 74

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122  
 DV +D E+ F I + VG I G+ H IAFAN E+L G + T+R+GFLLA +ISS  
 Sbjct: 75 LPCDVTNDAEIETCFASIKEQVGVIIHGIAHCIAFANKEELVGEYLNTNRDGFLLAHNIISS 134

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YSLT V A+ +M EGGSIV TYLGGE + NYNVMGVAKASL+A+VKYLA DLG +N  
 Sbjct: 135 YSLTAVVKAARPMMTEGGSIVTLYLGELVMPNYNVMGVAKASLDASVKYLAADLGKEN 194

Query: 183 IRVNAISAGPIRTLSAKGVGGFTNITKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 IRVN+ISAGPIRTLSAKG+ FN+ILK+IEERAPL+R EVG TAA+L SD+S G+T  
 Sbjct: 195 IRVNSISAGPIRTLSAKGISDFNSILKDIEERAPLRTTPEEVGDTAAFLFSDMSRGIT 254

Query: 243 GENIHVDSGFH 253  
 GEN+HVDSGFH  
 Sbjct: 255 GENLHVDSGFH 265

[>gi|23097678|ref|NP\_691144.1| enoyl-[acyl-carrier protein] reductase [Oceanobacillus HTE831]  
 gi|22775901|dbj|BAC12179.1| enoyl-[acyl-carrier protein] reductase [Oceanobacillus Length = 258

Score = 248 bits (633), Expect = 6e-65  
 Identities = 135/252 (53%), Positives = 170/252 (67%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 LE K V+MG+AN+RSIA+G+ K L GA L+FTY + + +  
 Sbjct: 5 LEGKNIVVMGVANERSIAWGITKSLHNAGANLIFTNRQERSYQKLVKLLDKHEIQAKLIV 64

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 DV DE + F +IG+ VG I GV HS+AFAN ++L+G ++ TSR+GFLLAQ+IS+Y  
 Sbjct: 65 SCDVADDESIQQAFNEIGEKVGVIHGVVHSVAFANRDELQGEYANTSRDGFLLAQEISAY 124

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPNI 183

SL V AK+LM EGG IV TYLG E + YNVMGVAKASLEA+V+YLA D+G I  
 Sbjct: 125 SLVAVTAKAELMTEGGGIVTQTYLGAERVIPGYNVMGVAKASLEASVRYLAEDMGKYGI 184

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVTG 243  
 RVNA+SAGPIRTLSAKGV FN I E+APL+RNVDQ EVG +L+S+++ G+TG  
 Sbjct: 185 RVNAVSAGPIRTLSAKGVSNFNEKANVIVEKAPLRRNVDQDEVGDATLFLVSEMARGITG 244

Query: 244 ENIHVDMSGFHAI 255  
 E +HVDSGFH I  
 Sbjct: 245 EVLHVDSGFHII 256

[>gi|16800038|ref|NP\_470306.1| similar to enoyl- acyl-carrier protein reductase  
gi|25283456|pir||AH1553 enoyl- acyl-carrier protein reductase homolog lin0969 [im  
 Listeria innocua (strain Clip11262)]  
gi|16413428|emb|CAC96200.1| similar to enoyl- acyl-carrier protein reductase [Lis  
 Length = 262

Score = 244 bits (624), Expect = 7e-64  
 Identities = 135/258 (52%), Positives = 173/258 (67%), Gaps = 4/258 (1%)

Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLKVFTYXXXXXXXXXXXXQLNQ--PE 59  
 L+LE KTYV+MG+ANKRSIA+ +A+ L++ GAKLKVFTY LN+ +  
 Sbjct: 3 LSLEGKTYVVMGVANKRSIAWAIARSLNEAGAKLKVFTYADDRAKKSITELVPSLNEINQD 62

Query: 60 AHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLGRGFSETSREGFLLAQD 119  
 + DV S++ + FE I G + G+ H IAFAN + L G + E R+ FL A +  
 Sbjct: 63 PLILACDVTSEDAITATFETIKDKAGKLSGLAHCIAFANKDYLTDYLEVDRKSFLQAH 122

Query: 120 ISSYSLTIVAHAKKL--MPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALD 177  
 IS+YS T VA K L + E S++ TYLGGE V+NYN+MGVAKASL+A+V+YLA+D  
 Sbjct: 123 ISAYSFTAVARALKHLDMLTEDASLLTLYLGGERVVENVNIMGVAKASLDASVRYLAMD 182

Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDL 237  
 LG +RVNAISAGPIRT+SA+GV GF+ + +EERAPLKR EVG TA YL S+L  
 Sbjct: 183 LGAIGVRVNAISAGPIRTVSARGVSGFSDSISLVEERAPLKRATQAEVGDTAYYLFSLN 242

Query: 238 SSGVTGENIHVDMSGFHAI 255  
 S GVTGE IHVDSG+H I  
 Sbjct: 243 SRGVTGEVIHVDSGYHII 260

[>gi|16803010|ref|NP\_464495.1| similar to enoyl- acyl-carrier protein reductase  
 monocytogenes EGD-e]  
gi|25283455|pir||AB1196 enoyl- acyl-carrier protein reductase homolog lmo0970 [im  
 Listeria monocytogenes (strain EGD-e)]  
gi|16410372|emb|CAC99048.1| similar to enoyl- acyl-carrier protein reductase [Lis  
 monocytogenes]  
 Length = 262

Score = 244 bits (623), Expect = 9e-64  
 Identities = 135/258 (52%), Positives = 173/258 (67%), Gaps = 4/258 (1%)

Query: 2 LNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLKVFTYXXXXXXXXXXXXQLNQPEAH 61  
 L+LE KTYV+MG+ANKRSIA+ +A+ L++ GAKLKVFTY L++ +  
 Sbjct: 3 LSLEGKTYVVMGVANKRSIAWAIARSLNEAGAKLKVFTYADDRAKKSITELVPSLSEVNQN 62

Query: 62 --LYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 + DV S+E + FE I G + G+ H IAFAN + L G + E R+ FL A +  
 Sbjct: 63 PLILACDVTSEEAITETFETIKDKAGKLSGLAHCIAFANKDFLTGDTLEVDRKSFLQAHE 122

Query: 120 ISSYSLTIVAHAKKL--MPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALD 177  
 IS+YS T VA K L + E S++ TYLGGE V+NYN+MGVAKASL+A+V+YLA+D  
 Sbjct: 123 ISAYSFTAVARALKHLEMLTEDASLLTLYLGGERVVENVNIMGVAKASLDASVRYLAMD 182

Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237  
 LG +RVNAISAGPIRT+SA+GV GF+ + +EERAPLKR EVG TA YL S+L  
 Sbjct: 183 LGAIGVRVNAISAGPIRTVSARGVSGFSDSISLVEERAPLKRATQAEVGDTAYYLFNSNL 242

Query: 238 SSGVTGENIHVDSGFHAI 255  
 S GVTGE IHVDSGF+H I  
 Sbjct: 243 SRGVTGEVIHVDSGYHII 260

[>]>gi|15420715|gb|AAK97428.1|AF382392\_4 enoyl carrier reductase [Trichodesmium sp.  
 gi|23042844|gb|ZP\_00074197.1| hypothetical protein [Trichodesmium erythraeum IMS1  
 Length = 258

Score = 239 bits (610), Expect = 3e-62  
 Identities = 125/253 (49%), Positives = 173/253 (68%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNL K ++ GIAN RSIA+G+A+ L + GA L TY +  
 Sbjct: 1 MLNLTKNVALVTGIANNRSIAWGLAQQLHKAGANLGVTYLPDDKGKFQKKVWELVEPLSP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 LY +VQ D++V F Q+G+ G +D + H +AFA E+L G FS T+REGF A +  
 Sbjct: 61 SLYLPCNVQDDQQVKQTFAQVGEKWKLDLILHCLAFAGKEELSGDFSNTTREGFTRALE 120

Query: 120 ISSYSLTIVAHAKKLMPPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 ISSYSL ++ +AK+LM EGGSIT+ +YLGG V+NYNVMG+AK++LE NV+YLA +LG  
 Sbjct: 121 ISSYSLIDLSSKAKELMTEGGSIITLSYLLGGVRVVRNYNVMGIAKSALEMNVRYLAAELG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239  
 P NIR+NAISAGPIRTL++ VGG ++ +E+ APL+R V Q+E+G TAA+L SDL+S  
 Sbjct: 181 PKNIRINAISAGPIRTLASSAVGGILDIMHHVEKVALRRTVTQIEIGNTAFLCSDLAS 240

Query: 240 GVTGENIHVDSGF 252  
 G+TG+ ++VD+G+  
 Sbjct: 241 GITGQVVYVDAGY 253

[>]>gi|23128764|gb|ZP\_00110603.1| hypothetical protein [Nostoc punctiforme]  
 Length = 258

Score = 236 bits (601), Expect = 3e-61  
 Identities = 129/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNL K ++ GIAN RSIA+G+A+ L + GA L TY +  
 Sbjct: 1 MLNLTKNVALVTGIANNRSIAWGLAQQLHKAGANLGVTYLPDERGKMEKKVAELVEPLNP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 L+ +VQ +E++ FE I + G +D + H +AFA+ +DL G FS+TSR GF A +

Objct: 61 SLFLPCNVQDEEQIQFTFETIREQWGKLDILIHCLAFASKDDLSGDFSQTSRSGFSTALE 120  
 Query: 120 ISSYSLTIVAH EAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS+YSL ++ AK LM EGGSIV TYLGG A+ NYNVMGVAKA LE +V+YLA +LG  
 Objct: 121 ISTYSLVQLSGAAKPLMTEGGSIVTLYLGGVRAIPNYNVMGVAKAGLEMSVRYLAAELG 180  
 Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDQVEVGKTAAYLLSDLSS 239  
 P NIRVNAISAGPIRTL++ VGG ++ +EE APL+R V Q+EVG TAA+L SDLSS  
 Objct: 181 PQNIRVNAISAGPIRTLASSAVGGILDIMHHVEEVAPLRRVTQLEVGNATAFLCSDLSS 240  
 Query: 240 GVTGENIHVDSGF 252  
 G+TG+ ++V+D+G+  
 Objct: 241 GITGQVLYVVDAGY 253

[>gi|13924473|gb|AAK49021.1|AF195898\_2 enoyl-[acyl-carrier-protein] reductase [S] Length = 258  
 Score = 234 bits (597), Expect = 1e-60  
 Identities = 129/253 (50%), Positives = 168/253 (66%), Gaps = 1/253 (0%)  
 Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 ML+L K ++ GIAN +SIA+G+A+ L GA + TY +  
 Objct: 1 MLDLTGKNALVTGIANNKSIAWGIAQQLHAAGANIGVTYLPDDKGRFEKKVGELVAPLNP 60  
 Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 L+ +VQ D +V FE + K+ G +D + H +AFAN EDL G FS+TSR+GF A D  
 Objct: 61 SLFLPCNVQDDAQVDQVFESVKKEWGKLDILIHCLAFANREDLTGDFSDTSRDGFNTALD 120  
 Query: 120 ISSYSLTIVAH EAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS+YSLT +A AK +M EGG+IV TYLGG + NYNVMGVAK++LE +V+YLA DLG  
 Objct: 121 ISAYSLTRLARGAKTVMTEGGAVTLYLGGVKVIPNYNVMGVAKSALEMSVRYLAADLG 180  
 Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVDQVEVGKTAAYLLSDLSS 239  
 P NIRVNAISAGPIRTL++ VGG ++ +E APL+R V Q EVG AA+L SDLSS  
 Objct: 181 PSNIRVNAISAGPIRTLASSAVGGILDIMHHVEATAPLRRVTQKEVGNAAFLCSDLSS 240  
 Query: 240 GVTGENIHVDSGF 252  
 GVTG+ ++VDSG+  
 Objct: 241 GVTGQVLYVDSGY 253

[>gi|23019970|ref|ZP\_00059677.1| hypothetical protein [Clostridium thermocellum ?] Length = 252  
 Score = 234 bits (596), Expect = 1e-60  
 Identities = 131/250 (52%), Positives = 169/250 (67%), Gaps = 6/250 (2%)  
 Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L NK ++MG+ NK SIA+G+ K + + GA ++ TY ++  
 Objct: 5 LGNKNILVMGVRNKSIAWGVKAVQEEGANVIITYQSEREKEGAEQLGAD-----SIF 58  
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 Q D+ SDEE+ + F I + G + G+ HSIA A EDL+ F TSREGF A +IS+Y  
 Objct: 59 QCDIISDEEINSLFAAIKEKYGVLHGLVHSIAHAKTEDLQNDFIYTSREGFAHAMNISAY 118  
 Query: 124 SLTIVAH EAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183

SL V+ AK+LM EGGS+ TY+G E + YNVMGVAKA+LEA+V+YLA DLG NI  
 Sbjct: 119 SLVAVSRGAKELMTEGGSIITLTYMGSEKVFKGYNVMGVAKAALEASVRYLAADLGEANI 178

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGP++TLSAKGV F IL + ++APLKRN+ Q ++GKTA YLLSDLSSGVTG  
 Sbjct: 179 RVNAISAGPVKTLASKGVKNFGDILDAPPKAPLKRNITQEDLGKTALEYLLSDLSSGVTG 238

Query: 244 ENIHVDMSGFH 253  
 E IHVDMSG++  
 Sbjct: 239 EVIHVDMSGYN 248

[gi|23475798|ref|ZP\_00131074.1] hypothetical protein [Desulfovibrio desulfuricar]  
 Length = 254

Score = 233 bits (593), Expect = 3e-60  
 Identities = 123/252 (48%), Positives = 167/252 (66%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L++K +I+G+AN +SIA+G+A+ GA+L F+Y +L +  
 Sbjct: 3 LKDKKILILGVANNKSIAYGIAQEFKAQGARLAFSYPGEAIQKRVDPISEELGG--EFTF 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 ++DV D +V + + G++D V HSIAFA EDL GRF +TSREGF LA DIS+Y  
 Sbjct: 61 RLDVTDDAQVAAAVRTVEEQWGSVDVVVHSIAFAQREDLHGRFIDTSREGFKLAMDISAY 120

Query: 124 SLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183  
 SL V + LM EGGS++ TY G + + NYNVMGVAKA+LEA+V+YLA D+G I  
 Sbjct: 121 SLVCVCKAFEPLMTEGGSVLTMTYYGSQKVITNYNVMGVAKAALEASVRYLAADMGERGI 180

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNA+SAGPI+TL+A G+ GF TIL IEE APL+RNV +VG+TA +L SDLS VTG  
 Sbjct: 181 RVNAVSAGPIKTLAASGISGFKTILNHIEHAPLRRNVTQDVGRTAVFLASDLGAVTG 240

Query: 244 ENIHVDMSGFHAI 255  
 E + VD+G++ +  
 Sbjct: 241 EVLFVDAGYNVM 252

[gi|6686259|sp|Q05069|FABI\_ANASP Enoyl-[acyl-carrier-protein] reductase [NADH]  
 enoyl-ACP reductase)  
 Length = 258

Score = 232 bits (591), Expect = 5e-60  
 Identities = 127/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNL K ++ GIAN RSIA+G+A+ L GA L TY +  
 Sbjct: 1 MLNLTKNVALVTGIANNRSIAWGLAQQLHAAGANLGITYLPDERGKFEKKVSELVEPLNP 60

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 L+ +VQ+DE++ + F+ I G +D + H +AFAN +DL G FS+TSR GF A D  
 Sbjct: 61 SLFLPCNVQNDEQIQTSTFDTIRDKWGRDLILHCLAFANRDLTGDFSQTSRAGFATALD 120

Query: 120 ISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS++SL ++ AK LM EGGS+ +YLGG AV NYNVMGVAKA LEA+V+YLA +LG  
 Sbjct: 121 ISTFSLVQLSGAAKPLMTEGGSIITLSYLGGRVAVPNYNVMGVAKAGLEASVRYLASELG 180

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSS 239  
 NIRVNAISAGPIRTL++ VGG ++ +E+ APL+R V Q+EVG TAA+L SDL+S  
 Sbjct: 181 SQNIRVNAISAGPIRTLASSAVGGILDIMHHVEQVAPLRRVTQLEVGNNTAAFLASLAS 240

Query: 240 GVTGENIHVDSGF 252  
 G+TG+ ++VD+G+  
 Sbjct: 241 GITGQVLYVDAGY 253

[>gi|17231883|ref|NP\_488431.1| enoyl-[acyl-carrier-protein] reductase [Nostoc sp. gi|25283464|pir||AG2354 enoyl-[acyl-carrier-protein] reductase [imported] - Nostoc (strain PCC 7120)  
 gi|142010|gb|AAD04184.1| unknown [Nostoc sp. PCC 7120]  
 gi|17133527|dbj|BAB76090.1| enoyl-[acyl-carrier-protein] reductase [Nostoc sp. PC Length = 264

Score = 232 bits (591), Expect = 5e-60  
 Identities = 127/253 (50%), Positives = 170/253 (67%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 MLNL K ++ GIAN RSIA+G+A+ L GA L TY +  
 Sbjct: 7 MLNLTKNVLVTGIANNRSIAWGIAQQLHAAGANLGITYLPDERGKFEKKVSELVEPLNP 66

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAQD 119  
 L+ +VQ+DE++ + F+ I G +D + H +AFAN +DL G FS+TSR GF A D  
 Sbjct: 67 SLFLPCNVQNDEQIQSTFDTIRDKWGRLDILIHCLAFANRDLTGDFSQTSRAGFATALD 126

Query: 120 ISSYSLTIVVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS++SL ++ AK LM EGGS+ +YLGG AV NYNVMGVAKA LEA+V+YLA +LG  
 Sbjct: 127 ISTFSLVLQQLSGAAKPLMTEGGSIITLSYLGGVRAVPNQVMGVAKAGLEASVRYLASELG 186

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSS 239  
 NIRVNAISAGPIRTL++ VGG ++ +E+ APL+R V Q+EVG TAA+L SDL+S  
 Sbjct: 187 SQNIRVNAISAGPIRTLASSAVGGILDIMHHVEQVAPLRRVTQLEVGNNTAAFLASLAS 240

Query: 240 GVTGENIHVDSGF 252  
 G+TG+ ++VD+G+  
 Sbjct: 247 GITGQVLYVDAGY 259

[>gi|23122150|gb|ZP\_00104285.1| hypothetical protein [Prochlorococcus marinus subsp. CCMP1378]  
 Length = 260

Score = 224 bits (572), Expect = 7e-58  
 Identities = 121/255 (47%), Positives = 172/255 (67%), Gaps = 4/255 (1%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQP-- 58  
 +LNL K ++ GIAN RSIA+G+A+ L + GA+L TY +L QP  
 Sbjct: 2 LLNLSGKKILVTGIANNRSIAWGIAQQLSKAGAELGITY-LPDDKGRFESKVRELTQPLN 60

Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAQ 118  
 + +DVQ+ ++ F+ I + G IDG+ H +AFA ++L G +S T+ EGF A  
 Sbjct: 61 PSLFLPLDVQNPAQIEEIFKNIKDNWQIDGLVHCLAFAGRDELIGDYSATTSEGFDRAL 120

Query: 119 DISSYSLTIVVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDL 178

+IS+YSL + AK L +G +V+ TYLG E A+ NYNVMGVAKA+LEA+V+YL+ +L  
 Sbjct: 121 NISAYSLAPLCKAAKPLFSDGAGVVSILTYLGSERAIPNYNVMGVAKAALEASVRYLSAEL 180

Query: 179 GPD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDVQEVGKTAAYLLSDL 237  
 GP+ +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q EVG TAA+LLSDL  
 Sbjct: 181 GPEKQVRVNAISAGPIRTLASSAIGGILDIMHNVEEKAPLRRVTQTEVGNTAAFLSDL 240

Query: 238 SSGVTGENIHVDMSGF 252  
 SSG++G+ I+VD+G+  
 Sbjct: 241 SSGISGQTIYVDAGY 255

[>]>gi|23132326|gb|ZP\_00114111.1| hypothetical protein [Prochlorococcus marinus str  
 Length = 268

Score = 224 bits (571), Expect = 9e-58  
 Identities = 119/254 (46%), Positives = 168/254 (66%), Gaps = 2/254 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 +L+L K ++ GIAN RSIA+G+A+ L GA+L TY E  
 Sbjct: 10 LLDLSGKKILVTGIANNRSIAWGLAQQLKAAGAELGITYLADERGRSEGVKVRDLTAPLEP 69

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 L+ ++VQ ++ F I + G +DG+ H +AFA E+L G +S TS EGF A +  
 Sbjct: 70 SLFLPLNVQDSNQIEEVFAVIAQQWGQLDGLVHCLAFAGKEELVGDYSATSAEGFARALE 129

Query: 120 ISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS+YSL + H AK L +G +V TYLG + A+ NYNVMGVAKA+LEA+V+YL+ +LG  
 Sbjct: 130 ISAYSLAPLCHHAKPLFSDGAGVVTLYLGADRAIPNPNVMGVAKAALEASVRYLSAELG 189

Query: 180 PD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDVQEVGKTAAYLLSDL 238  
 PD +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q+EVG TAA+LLSDL  
 Sbjct: 190 PDKQVRVNAISAGPIRTLASSAIGGILEMIHNVEEKAPLRRVTQIEVGNTAAFLSDL 249

Query: 239 SGVTGENIHVDMSGF 252  
 SG++G+ ++VD+G+  
 Sbjct: 250 SGISGQTLYVDAGY 263

[>]>gi|23110472|gb|ZP\_00096626.1| hypothetical protein [Novosphingobium aromaticivorans]  
 Length = 481

Score = 224 bits (571), Expect = 1e-57  
 Identities = 117/252 (46%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K +IMG+AN +S+A+G+AK L + GA+L F+Y L L  
 Sbjct: 219 MQGKRGGLIMGLANDKSLAWGIAKKLHEQGAELAFSYQGEALEKVRVPLAESLGSD--FLI 276

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 + DV + FE + ID + H+I +++ LRG+F +T+ + FL+ +IS+Y  
 Sbjct: 277 ECDVSDMAALDQTFETLKARWPTIDFIVHAIGYSDKNQLRGKFYDTTLDNFLMTMNISAY 336

Query: 124 SLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
 SL V A ++MP GGSI+ TY G E V +YNVMGVAKA+LEA+VKYLA D GP I  
 Sbjct: 337 SLVAVTKRAAEMMPAGGSILTLTYYGAEKVVPHYNVMGVAKAALEASVKYLANDCGPAGI 396

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVVG 243

RVNAISAGPI+TL+A G+G F ILK E +PL+RNV +VG Y LSDLSSGVVG

Sbjct: 397 RVNAISAGPIKTLAASGIGDFRYILKWNELNSPLRRNVTIEDVGGAGLYFLSDLSSGVVG 456

Query: 244 ENIHVDMSGFHAI 255

E HVD+G+H +

Sbjct: 457 ETHHVDAGYHTV 468

[>gi|22299236|ref|NP\_682483.1| enoyl-[acyl-carrier-protein] reductase [Thermosyne elongatus BP-1]  
gi|22295418|dbj|BAC09245.1| enoyl-[acyl-carrier-protein] reductase [Thermosynecho elongatus BP-1]  
Length = 259

Score = 221 bits (562), Expect = 1e-56

Identities = 123/253 (48%), Positives = 161/253 (63%), Gaps = 1/253 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTY-XXXXXXXXXXXXQLNQPE 59  
+L+L K ++ GIAN RSIA+G+A+ + GA+L TY

Sbjct: 2 LLDLSGKRALVTGIANNRSIAWGIAQQIHAAGAELAVTYLPDERGKLQKVEELTAPLVP 61

Query: 60 AHLYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
L +DVQ +++ + F I G +D + H +AFA EDL G FS S EGF LA D

Sbjct: 62 KLLLPLDVQQPQQIDDVFAAIQSTWGGLDILIHCLAFQAQKEDLNGDFSAVSLEGFHLALD 121

Query: 120 ISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
IS+YSL ++ AK LM GGSI+ TYLGG V NYNVMG+AKA+LE NV+YLA +LG

Sbjct: 122 ISAYSLISLSRAAKPLMTHGGSIITLTYLGGVRVVPNPNVNGIAKAALEMNVRYLAAELG 181

Query: 180 PDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSS 239  
P NIRVN ISAGPIRTL++ VGG ++ +E APL+R V Q EVG TAA+L SDL+S

Sbjct: 182 PRNIRVNGISAGPIRTLASSAVGGILDIMHHVEATAPLRRVTQTEVGNTAAFLASLAS 241

Query: 240 GVTGENIHDMSGF 252

G+TG+ ++VDSG+

Sbjct: 242 GITGQILYVDSGY 254

[>gi|15964651|ref|NP\_385004.1| PUTATIVE ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE NADH  
meliloti]  
gi|17366329|sp|P58380|FAI1\_RHIME Enoyl-[acyl-carrier-protein] reductase [NADH] 1  
enoyl-ACP reductase 1)  
gi|15073829|emb|CAC45470.1| PUTATIVE ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE NADH [S  
meliloti]  
Length = 272

Score = 219 bits (557), Expect = 4e-56

Identities = 126/253 (49%), Positives = 164/253 (64%), Gaps = 4/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA-HL 62  
+ K VIMG+AN RSIA+G+AK L + GA++ T+ +L A H

Sbjct: 8 MNGKRGVIMGVANNRSIAWGIAKALAEAGAEIALTWQGDALKRVEPLAQUELGAFMAGHC 67

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122  
D+ + + V + E+ G ID V H+IAF++ ++L GR+ +TSR+ F DIS

Sbjct: 68 DVTDLATIDAVFSALEE---KGKIDFVVHIAFSDKDELTGRYLDTSRDNFARTMDISV 124

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YS T VA A ++M +GGSI+ TY G E + +YNVMGVAKA+LEA+V+YLA+DLG  
 Sbjct: 125 YSFTAVAARADRVMDGGSILTLTYYGAEKVMPHYNVMGVAKAALEASVRYLAVDLGNRG 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDQVEVGKTAAYLLSDLSSGVT 242  
 IRVNAISAGPI+TL+A G+G F ILK E APLKR V EVG +A YLLSDLSSGVT  
 Sbjct: 185 IRVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLKRTVSIEEVGNSALYLLSDLSSGVT 244

Query: 243 GENIHVDSGFHAI 255  
 GE HVDSG+H +  
 Sbjct: 245 GEVHHVDSGYHTV 257

[>gi|22958522|gb|ZP\_00006191.1] hypothetical protein [Rhodobacter sphaeroides]  
 Length = 274

Score = 218 bits (556), Expect = 5e-56  
 Identities = 115/252 (45%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K +IMG+AN +SIA+G+AK GA+L F+Y + E +  
 Sbjct: 6 LAGKRGGLIMGLANDKSIAWGIAKCCADQGAEELAFSYQGDALKRVEPLAASIGATE--MV 63

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAQDISSY 123  
 + DV + + F + + G +D V H+I F++ +LRGR+ +T+ F + DIS Y  
 Sbjct: 64 ECDVSDEASLDRLFAHLKEVWGTLDVVHAIGFSKSELRGRYVDTTPANFRMTMDISVY 123

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPNI 183  
 S T V A +MP GGS++ TY G E + +YNVMG+AKA+LE +V+Y+A DLG D I  
 Sbjct: 124 SFTAVCQRACAMMPAGGSLLTLYGAEKVMPHYNVMGIAKAALETSVQYIAEDLGKDGI 183

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDQVEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGPI+TL+A G+G F I+K E +PL+RNV Q EVGK A YLLSDL SG TG  
 Sbjct: 184 RVNAISAGPIKTLAASGIGDFRYIMKWNELNSPLRRNVTQEEVGKAALYLLSDLGSGTTG 243

Query: 244 ENIHVDSGFHAI 255  
 E +HVD+G+H +  
 Sbjct: 244 EVLHVDAGYHVV 255

[>gi|22963177|gb|ZP\_00010783.1] hypothetical protein [Rhodopseudomonas palustris]  
 Length = 273

Score = 218 bits (556), Expect = 6e-56  
 Identities = 124/252 (49%), Positives = 160/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K VI+G+AN RSIA+G+AK GA++ TY +L L  
 Sbjct: 8 MQGKRGVILGVANNRSIAWGIAKACRAQGAEIALTYQGDALKRVEPLAELGG--LVLG 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLAQDISSY 123  
 DV + F+ + G ID V H+IAFA+ ++L GR+ +TS E F + IS Y  
 Sbjct: 66 HCDVTDGATIDAVFDAVKEKWGKIDFVVHAIADFADKDELDGRYVDTSPENFSKMLISCY 125

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPNI 183  
 SLT +A A+KLM +GGSI+ TY G E + +YNVMGVAKA+LEA+V+YLA DLG NI

Sbjct: 126 SLTAIAQRAEKLMTDGGSIITLTYYGAEKWMRPHYNVMGVAKAALEASVRYLAADLGEKNI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVTG 243  
RVNAISAGPI+TL+A G+G F ILK E APL+R V EVG +A Y LSDLS GVTG

Sbjct: 186 RVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLRTVTIEEVGDSALYFLSDLSRGVTG 245

Query: 244 ENIHVDMSGFHAI 255

E HVDSG+H +

Sbjct: 246 EVHHVDSGYHVV 257

[>gi|15888100|ref|NP\_353781.1| AGR\_C\_1374p [Agrobacterium tumefaciens]  
gi|17934667|ref|NP\_531457.1| enoyl-(acyl-carrier-protein) reductase [NADH] [Agrobacterium tumefaciens str. C58 (U. Washington)]  
gi|25283457|pir||E97451 hypothetical protein AGR\_C\_1374 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
gi|25283463|pir||AG2669 enoyl-(acyl-carrier-protein) reductase [NADH] fabI [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
gi|15155730|gb|AAK86566.1| AGR\_C\_1374p [Agrobacterium tumefaciens str. C58 (Cereon)]  
gi|17739126|gb|AAL41773.1| enoyl-(acyl-carrier-protein) reductase [NADH] [Agrobacterium tumefaciens str. C58 (U. Washington)]  
Length = 272

Score = 217 bits (553), Expect = 1e-55

Identities = 124/252 (49%), Positives = 161/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANRSIAFGVAKVLQAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
+ K +IMG+AN RSIA+G+AK GA+L T+ +L A

Sbjct: 8 MAGKRGGLIMGVANNRSIAWGIKACADAGELALTWQGDALKRVEPLAQELGAFMAG-- 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
DV E + + F + + G ID V H+IAF++ ++L GR+ +TSR+ F DIS +

Sbjct: 66 HCDVTDLETIDSFVASFLEQHWGKIDFVVHAIASFSDKDELTGRYLDTSRDNFNRTMDISVF 125

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
SL VA A+ +M +GGSI+ TY G E + NYNVMGVAKA+LEA+V+YLA+DLG I

Sbjct: 126 SLAAVAKRAEPIMNDDGGSIITLTYYGAEKVMRPNVVMGVAKAALEASVRYLAVDLGNRGI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVTG 243  
RVNA+SAGPI+TL+A G+G F ILK E APLKR V EVGK+A YLLSDL+ GVTG

Sbjct: 186 RVNAVSAGPIKTLAASGIGDFRYILKWNEYNAPLRTVTIEEVGKSALYLLSDLSTAVTG 245

Query: 244 ENIHVDMSGFHAI 255

E HVDSG+H I

Sbjct: 246 EIHHVDSGYHTI 257

[>gi|17987795|ref|NP\_540429.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella suis]  
gi|23501323|ref|NP\_697450.1| enoyl-(acyl-carrier-protein) reductase [Brucella suis]  
gi|25283461|pir||AB3441 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.1)  
[imported] - Brucella melitensis (strain 16M)  
gi|17983520|gb|AAL52693.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella suis]  
gi|23347213|gb|AAN29365.1|AE014352\_11 enoyl-(acyl-carrier-protein) reductase [Brucella suis]  
Length = 272

Score = 216 bits (550), Expect = 3e-55

Identities = 124/252 (49%), Positives = 157/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L+ K +I+G+AN RSIA+G+AK + GA+L FTY +L A  
 Sbjct: 8 LQGKRGGLILGVANNRSIAWGIAKAAREAGAELAFTYQGDALKRVEPLAELGAFVAG-- 65

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 DV + FE + K G +D + H+I F++ ++L GR+ +TS F IS Y  
 Sbjct: 66 HCDVADAASIDAVFETLEKKWGKLDFLVHAIGFSDKDELTGRYIDTSEANFTNTMLISVY 125

Query: 124 SLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPNI 183  
 SLT V+ A+KLM +GGSI+ TY G E + NYNVMGVAKA+LEA+VKYLA+DLGP NI  
 Sbjct: 126 SLTAWSRRAEKLMADEGGSILTLTYYGAEKVMPNYNVMGVAKAALEASVVKYLAVDLGPQNI 185

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGPI+TL+A G+G F ILK E APL+R V EVG Y LSDLS VTG  
 Sbjct: 186 RVNAISAGPIKTLAASGIGDFRYILKWNEYNAPLRRTVTIDEVGVDGLYFLSDLRSVTG 245

Query: 244 ENIHVDSGFHAI 255  
 E H DSG+H I  
 Sbjct: 246 EVHHADSGYHVI 257

[>gi|13476200|ref|NP\_107770.1| enoyl-acyl carrier protein reductase [Mesorhizobium  
 gi|14026960|dbj|BAB53556.1| enoyl-acyl carrier protein reductase [Mesorhizobium 1  
 Length = 272

Score = 216 bits (549), Expect = 4e-55  
 Identities = 122/253 (48%), Positives = 161/253 (63%), Gaps = 4/253 (1%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHL 62  
 + K +I+GIAN RSIA+G+AK GA++ TY +L A H  
 Sbjct: 8 MAGKRGGLILGIANNRSIAYGIAKACVDHGAEIALTYQGEAFKKRVEPLAELGAFVAGHC 67

Query: 63 YQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISS 122  
 D S +EV F + K G +D + H+IAF++ ++L GR+ ET+R+ FL DIS  
 Sbjct: 68 DVTDSASLDEV---FANVAKHWGKLDFLVHAIAFSDKDELTGRYVETTRDNFLRTMDISV 124

Query: 123 YSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPNI 182  
 +S T +A A+ LM EGGS++ TY G E + +YNYVMGVAKA+LEA+V+YLA+DLG  
 Sbjct: 125 FSFTTIAKRAEALMTEGGSLLTLYGAEKVMPHYNVMGVAKAALEASVRYLAVDLGGKK 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVT 242  
 IRVNAISAGPI+TL+A G+G F ILK E +PLK+ V Q EVG + Y LSDLS GVT  
 Sbjct: 185 IRVNAISAGPIKTLAASGIGDFRYILKWNEYNSPLKQTVQEEVGDSGVYFLSDLRSRGVT 244

Query: 243 GENIHVDSGFHAI 255  
 GE HVDSG+H +  
 Sbjct: 245 GEVHHVDSGYHVV 257

[>gi|23132906|ref|ZP\_00114680.1| hypothetical protein [Synechococcus sp. WH 8102]  
 Length = 260

Score = 214 bits (546), Expect = 7e-55  
 Identities = 116/254 (45%), Positives = 167/254 (65%), Gaps = 2/254 (0%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEA 60  
 +L+L K ++ GIAN RSIA+G+A+ L GA+L TY E  
 Sbjct: 2 LLDLTGKKILVTGIANNRSIAWGLIAQQLKAAGAELGITYLPDDKGRFEAKVRELTAPLEP 61

Query: 61 HLY-QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQD 119  
 L+ ++VQ +++ F +I G +DG+ H +AFA E+L G +S T+ EGF + D  
 Sbjct: 62 SLFLPLNVQDADQMAEVFGEIKAKWGVLDGLVHCLAFAGKEELIDYSATTAEGFARSLD 121

Query: 120 ISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLG 179  
 IS+YSL + AK L E ++ +YLG E A+ NYNVMGVAKA+LEA+V+YLA +LG  
 Sbjct: 122 ISAYSLAPLCAHAKPLFSEKAGVITLSYLGAEVPAIPNYNVMGVAKAALEASVRYLAAELG 181

Query: 180 PD-NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDQVEVGKTAAYLLSDL 238  
 P+ +RVNAISAGPIRTL++ +GG ++ +EE+APL+R V Q+EVG TAA+LLSDL+  
 Sbjct: 182 PEKQVRVNAISAGPIRTLASSAIGGILDIMIHNVEEKAPLRRVTQMEVGGTAAFLLSDL 241

Query: 239 SGVTGENIHVDMSGF 252  
 SG++G+ I+VD+G+  
 Sbjct: 242 SGISGQTIYVDAGY 255

► >gi|16329628|ref|NP\_440356.1| enoyl-[acyl-carrier-protein] reductase [Synechocystis sp. (strain PCC 6803)]  
 gi|7427661|pir||S74996 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9)  
 gi|1652111|dbj|BAA17036.1| enoyl-[acyl-carrier-protein] reductase [Synechocystis sp. (strain PCC 6803)]  
 Length = 278

Score = 214 bits (545), Expect = 1e-54  
 Identities = 120/254 (47%), Positives = 160/254 (62%), Gaps = 3/254 (1%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQ-- 58  
 ML+L K + GIAN RSIA+G+A+ L Q GA++ +Y +L +P  
 Sbjct: 21 MLDLSGKHAFTVGIANNRSIAWGLIAQQLHQAGAEIGVSY-LPDEKGRFEKKVRELTEPLH 79

Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQ 118  
 + DVQ D +V F ++ G +D + H +AFA+ L G +++ +E F A  
 Sbjct: 80 PTLVLPGDVQDDAQVDALFHSVKEKWGKLDILIHCLAFADKSLGTGNYTDIPKEAFSQAM 139

Query: 119 DISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDL 178  
 +IS+YSL +A AK LM GGSI+ TY GG + NYN+MGVAKA LE V+YLA +L  
 Sbjct: 140 EISTYSLGRLARGAKPLMTNGGSIITLTYFGGVKVIPNYNLMGVAKAGLEMTVRYLAAEL 199

Query: 179 GPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQDQVEVGKTAAYLLSDL 238  
 GP NIRVN ISAGPIRTL++ VGG ++ +EE APLKR V Q EVG TAA+L SDLS  
 Sbjct: 200 GPQNIRVNGISAGPIRTLASSAVGGILDIMIHHVEEVPLKRTVTQTEVGNTAAFLSDL 259

Query: 239 SGVTGENIHVDMSGF 252  
 SG+TG+ I+VDMSG+  
 Sbjct: 260 SGITGQIIYVDMSGY 273

► >gi|6685443|sp|P73016|FABI\_SYN3 Enoyl-[acyl-carrier-protein] reductase [NADH]  
 enoyl-ACP reductase)  
 Length = 258

Score = 214 bits (544), Expect = 1e-54  
 Identities = 120/254 (47%), Positives = 160/254 (62%), Gaps = 3/254 (1%)

Query: 1 MLNLENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQP-- 58  
 ML+L K + GIAN RSIA+G+A+ L Q GA++ +Y +L +P  
 Sbjct: 1 MLDLSGKHAFVTGIANNRSIAWGIAQQLHQAGAEIGVSY-LPDEKGRFEKKVRELTEPLH 59

Query: 59 EAHLYQIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLAQ 118  
 + DVQ D +V F + + G +D + H +AFA+ L G +++ +E F A  
 Sbjct: 60 PTLVLPGDVQDDAQVDALFHSVKEKGKLDILIHCLAFADKSGLTGNYTDIPKEAFSQAM 119

Query: 119 DISSYSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDL 178  
 +IS+YSL +A AK LM GGSI+ TY GG + NYN+MGVAKA LE V+YLA +L  
 Sbjct: 120 EISTYSLGRLARGAKPLMTNGGSIITLTYFGGVKVIPNYNLMGVAKAGLEMTVRYLAAEL 179

Query: 179 GPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLS 238  
 GP NIRVN ISAGPIRTL++ VGG ++ +EE APLKR V Q EVG TAA+L SDLS  
 Sbjct: 180 GPQNIRVNGISAGPIRTLASSAVGGILDIMIHVEEVAPLKRTVTQTEVGNTAAFLASDLS 239

Query: 239 SGVTGENIHVDMSGF 252  
 SG+TG+ I+VDSG+  
 Sbjct: 240 SGITGQIYVDSGY 253

[...]>gi|22966064|gb|ZP\_00013661.1| hypothetical protein [Rhodospirillum rubrum]  
 Length = 339

Score = 213 bits (542), Expect = 2e-54  
 Identities = 116/253 (45%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K + +G+AN RSIA+G+AK GA + FTY L+ E HL  
 Sbjct: 68 LAGKKGLVLGVANDRSIAWGIAKAASDAGASIAFTYQGDPLLKRVKPLVEGLS--ERHLL 125

Query: 64 QIDVQSDEEVING-FEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLAQDISS 122  
 +DE ++ F + + G ID V H++AF++ + L+G + T+RE F IS  
 Sbjct: 126 MPCDVTDEASLDAVFATLKETWGTIDFVVHAVAFAFSQDKDQLKGH YMHTRENFQOTMLISV 185

Query: 123 YSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDGP DN 182  
 +S T +A A ++M +GG+++ TY G E + +Y NVMGVAKA+LEA+V+YLA DLG  
 Sbjct: 186 FSFTDIARRASEIMNDGGAMITLTYYGAERVMPHYNVVMGVAKAALEASVRYLAADLGGRG 245

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQEVGKTAAYLLSDLSSGVT 242  
 IRVNAISAGPI+TL+A G+G F ILK E +PL+RNV EVG + YLLSDLS GVT  
 Sbjct: 246 IRVNAISAGPIKTLAASGIGDFRYILKWNEYNSPLRRNVTIDEVGNSGLYLLSDLSRGVT 305

Query: 243 GENIHVDMSGFHAI 255  
 GE HVDMSG+H +  
 Sbjct: 306 GEVHHVDSGYHLV 318

[...]>gi|23055279|gb|ZP\_00081394.1| hypothetical protein [Geobacter metallireducens]  
 Length = 256

Score = 210 bits (534), Expect = 2e-53  
 Identities = 123/253 (48%), Positives = 163/253 (64%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L+ K VI GIAN++SIA+ +A+ + GA+L TY + + +

Sbjct: 4 LDGKKAVIFGIANEKSIAWAIAQAFRREGAELAVTYANETVAKRVIPLAESVGA--SLVL 61  
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
     DV++D E+ + FE+IGK G ID + HSIAFA E+L+G F T+REGF LA DIS+Y  
 Sbjct: 62 PCDVRNDAEIQSVDGEEIGKAWGGIDILVHSIAFAGKEELKGSFLNTTREGFALALDISAY 121  
 Query: 124 SLTIVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 182  
     SL + A M GS++A TY GG+ NYNVMGVAKA+LE +VKYLA +G D  
 Sbjct: 122 SLIALMKAAPFMAGREGSVLALTYGGQKVFPNPNVMGVAKAALEMSVKYLAEVGSDG 181  
 Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVT 242  
     IRVNAISAGP++TL++ GVGFn I + E+APL+RN+ Q EV A YL S L+SGV+  
 Sbjct: 182 IRVNAISAGPLKTLASSGVGGFNQIAGHVAEKPLRRNISQDEVAGAAVYLASSLASGVS 241  
 Query: 243 GENIHVDSGFHAI 255  
     GE VDSG++ I  
 Sbjct: 242 GEIHFVDSGYNII 254

□ >gi|27377740|ref|NP\_769269.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizobium japonicum]  
 gi|27350885|dbj|BAC47894.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizobium japonicum]  
 Length = 271

Score = 210 bits (534), Expect = 2e-53  
 Identities = 119/252 (47%), Positives = 158/252 (62%), Gaps = 4/252 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
     ++ K V++G+AN RSIA+G+AK GA+L FTY ++ L  
 Sbjct: 8 MQGKRGVVLGVANNRSIAWGIAKACHAAGAELAFTYQGDALKRVEPLAAEIGG--LVLG 65  
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
     DV + F + G ID + H+IA+ E L GR+ +T++E F + IS Y  
 Sbjct: 66 HCDVTDAATIDAFAVLKEKWGKIDFLVHAIAYG--EQLDGRYVDTTQENFSKMLISCY 123  
 Query: 124 SLTIVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
     S T VA A+KLM +GGS++ +Y G E + +YVMGVAKA+LEA+V+YLA DLG NI  
 Sbjct: 124 SFTAVAQRAEKLMTDGGSLITLSYYGAEKWMMPHYNVMGVAKAALEASVRYLAADLGEKNI 183  
 Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNDQVEVGKTAAYLLSDLSSGVTG 243  
     RVNAISAGPI+TL+A G+G F ILK E APL+RN+ +VG +A Y LSDLS GVTG  
 Sbjct: 184 RVNAISAGPIKTLAASGIGDFRYILKWNEHNAPLRRNVSTEDVGGSALYFLSDLRSRGVTG 243  
 Query: 244 ENIHVDSGFHAI 255  
     E HVDSG+H +  
 Sbjct: 244 EVHHVDSGYHVL 255

□ >gi|23059616|ref|ZP\_00084568.1| hypothetical protein [Pseudomonas fluorescens P1]  
 Length = 308

Score = 209 bits (532), Expect = 4e-53  
 Identities = 112/252 (44%), Positives = 155/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
     L K +I+G+A+K SIA G+A + + GA+L FTY +

Objct: 48 LAGKRVLIVGVASKLSIASGIAAMHREGAELAFTYQNDKLKGRVEEFAQQWGSSPELCF 107  
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
     DV SDEE+ FE++ K +D + HS+ FA + L G F+E T+REGF +A DIS+  
 Objct: 108 PCDVASDEEIAKVFEELSKWDGLDCIVHSGFAPGDQLDGFTEATTREGFRIAHDISA 167  
  
 Query: 123 YSLTIVAHAKKLMP-EGGSIVATTYLGGGEFAVQNYNVMGVAKASLEANVKYLALDLGPD 181  
     YS +A +++M GS++ +YLG E + NYNVMG+AKASLEA V+YLA LGPD  
 Objct: 168 YSFVALAKAGREMMKGRNGSLLTSLGAERTMPNYNVMGMAKASLEAGVRYLAGSLGPD 227  
  
 Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGV 241  
     RVN +SAGPIRTL+A G+ F +L E + PL+RNV EVG A+L SDL+SG+  
 Objct: 228 GTRVNCVSAGPIRTLAASGIKFRKMLAANEAQTPLRRNVTIEEVGNAGAFLCSDLASGI 287  
  
 Query: 242 TGENIHDVDSGFH 253  
     +GE ++VD GF+  
 Objct: 288 SGEIMYVDGGFN 299

[>gi|23015709|gb|ZP\_00055478.1] hypothetical protein [Magnetospirillum magnetotac]  
 Length = 289

Score = 208 bits (529), Expect = 7e-53  
 Identities = 115/258 (44%), Positives = 161/258 (62%), Gaps = 14/258 (5%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYYYYYYYYYYYYQLNQPEAHLY 63  
     + K ++MG+AN RSIA+G+A+ GA+L FTY +P A  
 Objct: 25 MAGKKGLVMGVANDRSIAWGLAQAAQGELAFTYQGEALEKRV-----RPLAQSV 76  
  
 Query: 64 QIDV----QSDEEVING-FEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLA 117  
     D+ SDE I+ F ++ K G +D V H+I +++ +LRGR+++TS + FL +  
 Objct: 77 GSDIVLPCDVSDEASIDAVFAELEKRWGKLDVFVHAIGYSDKNELRGYADTSQNFLTS 136  
  
 Query: 118 QDISSYSLTIVAHAKLMP EGGSIVATTYLGGGEFAVQNYNVMGVAKASLEANVKYLALD 177  
     IS +S T VA A +MP+GGS++ TY G E + +YNYVMG KA+LEA+V+YLA+D  
 Objct: 137 MHISVFSFTSVARRASAMMPDGGSLLTYYGAERVMPHYNVMGVCKAALEASVRYLAVD 196  
  
 Query: 178 LGPDNIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDL 237  
     LG IRVN++SAGPI+TL+A G+ F ILK E +PLKRNV ++G YLLS L  
 Objct: 197 LGGQGIRVNSLSAGPIKTLAASGIGDFRYILKWNEYNSPLKRNVTLEDIGGAGLYLLSGL 256  
  
 Query: 238 SSGVTGENIHDVDSGFHAI 255  
     SSGV+GE HVD G+H +  
 Objct: 257 SSGVSGETHHVDGCGYHVV 274

[>gi|22970115|gb|ZP\_00017264.1] hypothetical protein [Chloroflexus aurantiacus]  
 Length = 282

Score = 207 bits (528), Expect = 8e-53  
 Identities = 115/252 (45%), Positives = 157/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYYYYYYYYQLNQPEAHLY 63  
     +E K +I+G+AN RSIA+G+A+ L + GA + FTY LN P +  
 Objct: 26 MEGKKGLILGVANDRSIAWGLAQALHREGATIGFTYLGEALERRVRPLAESLNSP--LIV 83  
  
 Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123

DV DE++ EQ + G ID + H+IAFAN E+L G T+REGF +A +IS+Y  
 Sbjct: 84 PCDVSKDEDITALIEQARETFGQIDFLVHAIASFANKEELSGTILNTTREGFRIALEISAY 143

Query: 124 SLTIVVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
 SL + A+ + S++ TY G + +YNVMGVAKA+LEA+V+YLA LGP I  
 Sbjct: 144 SLIALVKAEEPIFAPPDASVLTLYHGARQVIGSYNVMGVAKAALEASVRYLAAGLGPRI 203

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGPIRTL+A G+ F ++ K E APL+RNV +VG A YL S L++GVTG  
 Sbjct: 204 RVNAISAGPIRTLAASGIANFRSLHKHFAEYAPLRRNVTIEDVGNAALYLCPLAAGVGTG 263

Query: 244 ENIHVDSGFHAI 255  
 E +VD+GF+ +  
 Sbjct: 264 EIHYVDAGFNVV 275

**gi|23103009|gb|ZP\_00089502.1| hypothetical protein [Azotobacter vinelandii]**  
 Length = 264

Score = 207 bits (527), Expect = 1e-52  
 Identities = 113/252 (44%), Positives = 156/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K +I+G+A+K SIA G+A + + GA+L FTY +  
 Sbjct: 4 LAGKRVLIVGVASKLSIASGIAAMHREGAELAFTYQNDKLKGRVEEFAAGWGSSPELCF 63

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 DV SDE++ FE++GK +D + HS+ FA + L G F+E TSR+GF +A DIS+  
 Sbjct: 64 PCDVASDEDIARVFEELGKKWDGLDCIVHSVGFAPGDQLNGDFTEVTSRDGFKIAHDISA 123

Query: 123 YSLTIVVAHEAKKLMP-EGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 181  
 YS +A ++LM GS++ +YLG E + NYNVMG+AKASLEA V+YLA LGP+  
 Sbjct: 124 YSFVALAKAGRELMKGRNGSLLTSLGAERTMPNVMGMAKASLEAGVRYLAASLGPE 183

Query: 182 NIRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 241  
 RVN ISAGPIRTL+A G+ F +L E + PL+RNV EVG A+L SDL+SG+  
 Sbjct: 184 GTRVNCISAGPIRTLAASGIASFRKMLAANERQTPLRRNVTIEEVGNAGAFLCSDLASGI 243

Query: 242 TGENIHVDSGFH 253  
 +GE ++VD GF+  
 Sbjct: 244 SGEILYVDGGFN 255

**gi|15602047|ref|NP\_245119.1| FabI [Pasteurella multocida]**  
**gi|12720402|gb|AAK02266.1| FabI [Pasteurella multocida]**  
 Length = 260

Score = 206 bits (523), Expect = 3e-52  
 Identities = 112/253 (44%), Positives = 159/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L NK +I G+A+ RSIA+G+A+ + + GA+L FTY +L +  
 Sbjct: 4 LTNKRILIAVGVASNRSAIYGIAQAMKREGAELAFTYQNDKLKGRVEEFAKELGSDI--VI 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 DV +DE + F ++ K DG HSIAFA + L G + + +REGF +A D+SS  
 Sbjct: 62 PCDVGTDESIEQCFAELAKHWEKFDGFVHSIAFAPGDQLDGDYDAVNREGFRIAHDVSS 121

Query: 123 YSLTIVAH EAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP DN 182  
 YS +A A+ ++ +++ +YLG E A+ NYNVMG+AKASLEAN +++A LG D  
 Sbjct: 122 YSFVAMAKAARGMLNPNSALLT SYLGAERAIPNYNVMGLAKASLEANTRFMAAALGKD G 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKR NVDQVEVGKTAAYLLSDLSSG VT 242  
 IRVNAISAGPIRTL+A G+ F +L E+ APL+R V +VG +AA+L SDLS+G+T  
 Sbjct: 182 IRVNAISAGPIRTLAASGIK NFKMLANFEQTAPL RRTVTIEDVGNSA AFLCS DLSAGIT 241

Query: 243 GENIHVDSSGFHAI 255  
 GE +HVD+GF +  
 Sbjct: 242 GEVVHVDAGFSIV 254

►>gi|13474637|ref|NP\_106206.1| enoyl-[acyl-carrier-protein] reductase [Mesorhizobium  
 gi|14025391|dbj|BAB51992.1| enoyl-[acyl-carrier-protein] reductase [Mesorhizobium  
 Length = 267

Score = 204 bits (519), Expect = 9e-52  
 Identities = 113/252 (44%), Positives = 156/252 (61%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIA NKR SIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K ++MG+AN SIA+G+AK L + GA+L FTY +L + +  
 Sbjct: 5 MKGKRG LVMGVANDHSIAWGIKKLSEHGAELAFTYQGDAFGR RVKPLADKLGA--SLVV 62

Query: 64 QIDVQSDEEVINGFEQIGKDVG NIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 DV+ V FE +GK+ G +D V H+I F++ +L+G +++TSR+ F+ IS Y  
 Sbjct: 63 PCDVEDSASVAATFETLGKEWGGLDFVVHAIGFS DKNELKGLYADTSRDNFVRTMVISCY 122

Query: 124 SLTIVAH EAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGP DN 183  
 S T VA A LM EGGS++ TY G + NYNVMG VAKA LEA+V+YLA D GP I  
 Sbjct: 123 SFTEVARNA AALMTEGGSMITLT YAGSVR VMPN YVMG VAKA GL EASVRYLANDY GPRGI 182

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKR NVDQVEVGKTAAYLLSDLSSG VT 243  
 RVN ISAGP+RTL+ G+ + +PL+R V EVG +A YLLSDL+SGVTG  
 Sbjct: 183 RVNGISAGPVRTLAGAGISDARHMFSYQQRNSPLRRTVTIDEVGGSALYLLSDLASGV TG 242

Query: 244 ENIHVDSSGFHAI 255  
 E +VDSG+H +  
 Sbjct: 243 EIHYVDSGYHIV 254

►>gi|17988241|ref|NP\_540875.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella suis]  
 gi|23503018|ref|NP\_699145.1| enoyl-(acyl-carrier-protein) reductase [Brucella suis]  
 gi|25283462|pir|AH3496 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.1)  
 [imported] - Brucella melitensis (strain 16M)  
 gi|17984008|gb|AAL53139.1| ENOYL-(ACYL-CARRIER-PROTEIN) REDUCTASE (NADH) [Brucella suis]  
 gi|23349059|gb|AAN31060.1|AE014503\_7 enoyl-(acyl-carrier-protein) reductase [Brucella suis]  
 Length = 272

Score = 204 bits (519), Expect = 1e-51  
 Identities = 118/253 (46%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIA NKR SIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K +IMG+AN S+A+G+AK L GA+L FTY Q+ +  
 Sbjct: 5 MQGKRG LIMGVANNHSLAWGIKQLAAQGAELAFTYQGDA LGKRVKPLAEQVGSD--FVL 62

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 DV+ V FE+I K G +D + H+I F++ +L+GR+++ T+RE F IS+  
 Sbjct: 63 PCDVEDIATVDAVFEEIEKKWGGFLVHAIGFSDKTELKGRYADVTTRENFSRTMVISA 122

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YS T VA A+KLM +GGSI+ TY G + NYNVMGVAKA+LEA V+YLA D GP  
 Sbjct: 123 YSFTEVAQRAEKKLMKDGGSLTLLTYGGSTRTIPNYNVMGVAKAALEAMVRYLAADYGPQG 182

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 IRVNAISAGP+RTL+ G+G I +PL+R VD +VGK+A YLLSDLSSGVT  
 Sbjct: 183 IRVNAISAGPVRTLAGAGIGDARAIFSYQRRNSPLRRTVDIDDVGKSAVYLLSDLSSGVT 242

Query: 243 GENIHVDSGFHAI 255  
 GE VDSG++ +  
 Sbjct: 243 GEIHFVDSGYNIV 255

[>gi|15792718|ref|NP\_282541.1| putative enoyl-[acyl-carrier-protein] reductase [Campylobacter jejuni]  
 gi|11250877|pir||H81284 probable enoyl-[acyl-carrier-protein] reductase (NADH2) (1.3.1.9) Cj1400c [imported] - Campylobacter jejuni (strain NCTC 11168)  
 gi|6968829|emb|CAB73824.1| putative enoyl-[acyl-carrier-protein] reductase [NADH] [Campylobacter jejuni subsp. jejuni NCTC 11168]  
 Length = 274

Score = 203 bits (517), Expect = 2e-51  
 Identities = 116/250 (46%), Positives = 163/250 (65%), Gaps = 2/250 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K +I+G+AN +SIA+G+AK GA+L FT+ + N +Y  
 Sbjct: 3 MKGKKGLIVGVANNKSIAYGIAKACFDQGAEALFTFLNDALKRVEPIAQEFNS--NFVY 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 ++DV ++E + + E+I KD+G ID V H++AFA E L F ETS+E F +A S Y  
 Sbjct: 61 ELDVNNNEHLDSSIAEKIKKDLGEIDFVVHAVAFAPEAKLENSFLETSKEAFDIAMQTSVY 120

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDNI 183  
 SL + ++ + GSI+ +YLGG V +YNYVMGVAKA+LE++V+YLA DLG I  
 Sbjct: 121 SLLSLTRAVLPILDKGSILTSLYLGGVKYVPHYNVMGVAKAALESSVRYLARDLGVKGI 180

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNAISAGP+TL+A G+G F ILK E +PLKRNV +VG +A YLLSDL++GVTG  
 Sbjct: 181 RVNAISAGPIKTLAASGIGDFRMLKYNEINSPLKRNVSIEDVGNSAMYLLSDLANGVTG 240

Query: 244 ENIHVDSGFH 253  
 E +VD+G++  
 Sbjct: 241 EIHYVDAGYN 250

[>gi|15611251|ref|NP\_222902.1| ENOYL-ACYL CARRIER PROTEIN REDUCTASE [Helicobacter]  
 gi|6685452|sp|Q9ZMN7|FABI\_HELPJ Enoyl-[acyl-carrier-protein] reductase [NADH] (NADH)  
 enoyl-ACP reductase)  
 gi|7431095|pir||B71964 enoyl-acyl carrier protein reductase - Helicobacter pylori  
 J99)  
 gi|4154700|gb|AAD05765.1| ENOYL-ACYL CARRIER PROTEIN REDUCTASE [Helicobacter pylori]

Length = 275

Score = 203 bits (516), Expect = 2e-51  
 Identities = 112/252 (44%), Positives = 160/252 (63%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSAIFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L+ K +I+G+AN +SIA+G+A+ GA L FTY +LN P ++Y  
 Sbjct: 4 LKGKKGLIVGVANNKSIAYGIAQSCFNQGATLAFTYLNESLEKRVRIAQELNSP--YVY 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 ++DV +E + + I +D+G++D + HS+AFA E L G ETS+ F A +IS Y  
 Sbjct: 62 ELDVSKKEHFKSLYNNNIQDLSLDFIVHSVAFAPKEALEGSLETSKSAFNTAMEISVY 121

Query: 124 SLTIVVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
 SL + + K L+ G S++ +YLG + +YNVMG+AKA+LE+ V+YLA+DLG NI  
 Sbjct: 122 SLIELTNTLKPPLLNGASVLTLSYLGSTKYMAYHNVMLAKAALESAVRYLAVDLGKHNI 181

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNA+SAGPIRTL++ G+ F ILK E APL++NV EVG YLLS LS+GV+G  
 Sbjct: 182 RVNALSAFPIRTLASSGIADFRMILKWNEINAPLRKNSLEEVGNAGMYLLSSLSNGVSG 241

Query: 244 ENIHVDSGFHAI 255  
 E VD+G+H +  
 Sbjct: 242 EVHFVDAGYHVM 253

►>gi|17545891|ref|NP\_519293.1| PROBABLE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [Ralstonia solanacearum]  
gi|17428186|emb|CAD14874.1| PROBABLE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH  
 OXIDOREDUCTASE [Ralstonia solanacearum]  
 Length = 264

Score = 203 bits (516), Expect = 2e-51  
 Identities = 115/251 (45%), Positives = 153/251 (60%), Gaps = 3/251 (1%)

Query: 4 LENKTYVIMGIANKRSAIFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K +I G+ + RSIA+G+A + GA+L FTY + + ++  
 Sbjct: 4 LAGKRILITGLLSNRSIAYGIASACKREGAELAFTYVGERFKDRITEFANEFGS--QLVF 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 DV SDE++ F +G+ + DG+ HSI FA E + G F + SRE F +A DIS+  
 Sbjct: 62 DCDVGSDEQIAKVFADLGQHWDHFGLVHSIGFAPREAIAGDFLDGLSREAFRIAHISA 121

Query: 123 YSLTIVVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 182  
 YS +A A ++ S++A TYLG E V NYN MGVAKA+LEA V+YLA LGP  
 Sbjct: 122 YSFPAKALPMLSPNASLLALTYLGAERVVPNYNTMGVAKAALEACVRYLASALGPKG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 IR N ISAGPI+TL+A G+ F +LK +E+ APL+RNV EVG AA+LLSDLSSG+T  
 Sbjct: 182 IRANGISAGPIKTLAASGIKDFGKLLKYMEDVAPLRRNVTIEEVGNVAAFLLSDLSSGMT 241

Query: 243 GENIHVDSGFH 253  
 GE +VD GF+  
 Sbjct: 242 GEITYVDCGFN 252

►>gi|26247623|ref|NP\_753663.1| Enoyl-[acyl-carrier-protein] reductase [NADH] [Esc

CFT073]

gi|26108025|gb|AAN80225.1|AE016760\_84 Enoyl-[acyl-carrier-protein] reductase [NAD  
CFT073]  
Length = 262

Score = 202 bits (514), Expect = 4e-51  
Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +  
Sbjct: 4 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDI--VL 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122  
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS  
Sbjct: 62 QCDVAEDTSIDTMFAELGKVWPKFDFGVHSIGFAPGDQLGDDYNAVTRREGFKIAHDISS 121

Query: 123 YSLTIVAHAEKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
Y S +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+  
Sbjct: 122 YSFVAMAKACRSMLNPGSALLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++  
Sbjct: 182 VRVNAISAGPIRTLAAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGIS 241

Query: 243 GENIHVDSGF 252  
GE +HVD GF  
Sbjct: 242 GEVVHVDGGF 251

►>gi|15801888|ref|NP\_287908.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli O157:H7 EDL933]  
gi|15831115|ref|NP\_309888.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli O157:H7]  
gi|16129249|ref|NP\_415804.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli K12]  
gi|24112687|ref|NP\_707197.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Shigella sonnei str. 301]  
gi|119391|sp|P29132|FABI\_ECOLI Enoyl-[acyl-carrier-protein] reductase [NADH] (NADH: enoyl-ACP reductase)  
gi|1073371|pir||S48029 enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) [Escherichia coli (strain K-12)]  
gi|25283445|pir||E90861 enoyl-[acyl-carrier-protein] reductase (NADH) ECs1861 [imported] [Escherichia coli (strain O157:H7, substrain RIMD 0509952)]  
gi|25283451|pir||H85757 enoyl-[acyl-carrier-protein] reductase (NADH) [imported] [Escherichia coli (strain O157:H7, substrain EDL933)]  
gi|9955169|pdb|1C14|A S Chain A, Crystal Structure Of E. Coli Enoyl Reductase-Nad+ Complex  
gi|9955170|pdb|1C14|B S Chain B, Crystal Structure Of E. Coli Enoyl Reductase-Nad+ Complex  
gi|20150083|pdb|1I2Z|A S Chain A, E. Coli Enoyl Reductase In Complex With Nad And Benzamide Inhibitor  
gi|20150084|pdb|1I2Z|B S Chain B, E. Coli Enoyl Reductase In Complex With Nad And Benzamide Inhibitor  
gi|20150085|pdb|1I30|A S Chain A, E. Coli Enoyl Reductase +nad+sb385826  
gi|20150086|pdb|1I30|B S Chain B, E. Coli Enoyl Reductase +nad+sb385826  
gi|23200396|pdb|1LX6|A S Chain A, Crystal Structure Of E. Coli Enoyl Reductase-Nad+ Complex

gi|23200397|pdb|1LX6|B **S** Chain B, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Benzamide Inhibitor  
gi|23200398|pdb|1LXC|A **S** Chain A, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Acrylamide Inhibitor  
gi|23200399|pdb|1LXC|B **S** Chain B, Crystal Structure Of E. Coli Enoyl Reductase-Na Bound Acrylamide Inhibitor  
gi|145851|gb|AAA17755.1| envM  
gi|587106|emb|CAA55381.1| enoyl-ACP reductase [Escherichia coli]  
gi|1787545|gb|AAC74370.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli K12]  
gi|12515500|gb|AAG56524.1|AE005378\_3| enoyl-[acyl-carrier-protein] reductase (NADH) [O157:H7 EDL933]  
gi|13361326|dbj|BAB35284.1| enoyl-[acyl-carrier-protein] reductase (NADH) [Escherichia coli O157:H7]  
gi|24051603|gb|AAN42904.1|AE015155\_11| enoyl-[acyl-carrier-protein] reductase (NAD str. 301)  
Length = 262

Score = 202 bits (513), Expect = 5e-51  
Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLVFTYXXXXXXXXXXQLNQPEAHLY 63  
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +  
Sbjct: 4 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDI--VL 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122  
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS  
Sbjct: 62 QCDVAEDASIDTMFAELGKVWPKFDFGVHSIGFAPGDQLGDDYNAVTRREGFKIAHDISS 121

Query: 123 YSLTIVAHAEKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
Y S +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+  
Sbjct: 122 YSFVAMAKACRSMLNPGSALLTSLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++  
Sbjct: 182 VRVNAISAGPIRTLAAASGIKDFRKMLAHCEAVPIRRTVTIEDVGNAAFLCSAGIS 241

Query: 243 GENIHVDSGF 252  
GE +HVD GF  
Sbjct: 242 GEVVHVDGGF 251

>gi|2914323|pdb|1DFG|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Benzo-Diazaborine  
gi|2914324|pdb|1DFG|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Benzo-Diazaborine  
gi|2914325|pdb|1DFH|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Thieno-Diazaborine  
gi|2914326|pdb|1DFH|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad And Thieno-Diazaborine  
gi|2914327|pdb|1DFI|A **S** Chain A, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad  
gi|2914328|pdb|1DFI|B **S** Chain B, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad  
gi|2914329|pdb|1DFI|C **S** Chain C, X-Ray Structure Of Escherichia Coli Enoyl Reductase-Na Bound Nad

gi|2914330|pdb|1DFI|D **S** Chain D, X-Ray Structure Of Escherichia Coli Enoyl Reduct Bound Nad  
gi|6137454|pdb|1QG6|A **S** Chain A, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan  
gi|6137455|pdb|1QG6|B **S** Chain B, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan  
gi|6137456|pdb|1QG6|C **S** Chain C, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan  
gi|6137457|pdb|1QG6|D **S** Chain D, Crystal Structure Of E. Coli Enoyl Acyl Carrier Reductase In Complex With Nad And Triclosan  
gi|6435557|pdb|1D8A|A **S** Chain A, E. Coli Enoyl ReductaseNAD+TRICLOSAN COMPLEX  
gi|6435558|pdb|1D8A|B **S** Chain B, E. Coli Enoyl ReductaseNAD+TRICLOSAN COMPLEX  
gi|1742101|dbj|BAA14841.11 Enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3. dependent enoyl-ACP reductase). [Escherichia coli]  
gi|1742110|dbj|BAA14849.11 Enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3. dependent enoyl-ACP reductase). [Escherichia coli]  
Length = 261

Score = 202 bits (513), Expect = 5e-51

Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRISIAFGVAKVLDQLGAKLVLFTYXXXXXXXXXXXXQLNQPEAHLY 63  
L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +

Sbjct: 3 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAQLGSDI--VL 60

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122  
Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS

Sbjct: 61 QCDVAEDASIDTMFAELGKVWPKFDFGVHSIGFAPGDQLDGDYVNAVTREGFKIAHDISS 120

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
Y S +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+

Sbjct: 121 YSFVAMAKACRSMLNPGSALLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 180

Query: 183 IRVNAISAGPIRTLASKVGGFTNILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
+RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++

Sbjct: 181 VRVNAISAGPIRTLAAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLASAGIS 240

Query: 243 GENIHVDSGF 252  
GE +HVD GF

Sbjct: 241 GEVVHVDGGF 250

>gi|5822339|pdb|1QSG|A **S** Chain A, Crystal Structure Of Enoyl Reductase Inhibition Triclosan  
gi|5822340|pdb|1QSG|B **S** Chain B, Crystal Structure Of Enoyl Reductase Inhibition Triclosan  
gi|5822341|pdb|1QSG|C **S** Chain C, Crystal Structure Of Enoyl Reductase Inhibition Triclosan  
gi|5822342|pdb|1QSG|D **S** Chain D, Crystal Structure Of Enoyl Reductase Inhibition Triclosan  
gi|5822343|pdb|1QSG|E **S** Chain E, Crystal Structure Of Enoyl Reductase Inhibition Triclosan  
gi|5822344|pdb|1QSG|F **S** Chain F, Crystal Structure Of Enoyl Reductase Inhibition Triclosan

gi|5822345|pdb|1QSG|G **[S]** Chain G, Crystal Structure Of Enoyl Reductase Inhibition  
 Triclosan  
gi|5822346|pdb|1QSG|H **[S]** Chain H, Crystal Structure Of Enoyl Reductase Inhibition  
 Triclosan  
 Length = 265

Score = 202 bits (513), Expect = 5e-51  
 Identities = 109/250 (43%), Positives = 155/250 (62%), Gaps = 3/250 (1%)

Query: 4 LENKTYVIMGIANKRSAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K ++ G+A+K SIA+G+A+ + + GA+L FTY QL +  
 Sbjct: 7 LSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDI--VL 64

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRF-SETSREGFLLAQDISS 122  
 Q DV D + F ++GK DG HSI FA + L G + + +REGF +A DISS  
 Sbjct: 65 QCDVAEDASIDTMFAELGKVWPKFDFVHSIGFAPGDQLDGYVNAVTREGFKIAHDISS 124

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YS +A + ++ G +++ +YLG E A+ NYNVMG+AKASLEANV+Y+A +GP+  
 Sbjct: 125 YSFVAMAKACRSMLNPGSALLTSLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEG 184

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 +RVNAISAGPIRTL+A G+ F +L E P++R V +VG +AA+L SDLS+G++  
 Sbjct: 185 VRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLISAGIS 244

Query: 243 GENIHVDSGF 252  
 GE +HVD GF  
 Sbjct: 245 GEVVHVDGGF 254

>gi|15672548|ref|NP\_266722.1| NADH-dependent enoyl-ACP reductase [Lactococcus lactis]  
gi|25283448|pir|F86695 NADH-dependent enoyl-ACP reductase fabI [imported] - Lact lactis subsp. lactis (strain IL1403)  
gi|12723453|qb|AAK04664.1|AE006290\_9| NADH-dependent enoyl-ACP reductase [Lactococ lactis]  
 Length = 250

Score = 201 bits (512), Expect = 7e-51  
 Identities = 113/250 (45%), Positives = 158/250 (63%), Gaps = 4/250 (1%)

Query: 4 LENKTYVIMGIANKRSAFGVAKVLDQLGAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 LE K VIMG+AN +SIA+G AK + GA L++TY +L +PE L  
 Sbjct: 3 LEGKKIVIMGVANNKSIAWGCAKAMDQGATIYTY---QNERMEKQLAKLAEPEDELLI 58

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 + DV SDE + F I VG IDG+ H+IA++ E+L G ++ SR+G+ LAQDIS+Y  
 Sbjct: 59 ECDVTSDESIRRAFGTIEARVGKIDGLVHAIAYSKEELGGNVTDISRDGYALAQDISAY 118

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
 SL VA AK L+ +G IV TY+G A+ NYNVMG+AKA+LE+ V+YLA ++ +  
 Sbjct: 119 SLLAVAKAAKPLLKKGSGIVTLYMGSVRAIPNYNVMGIAKAALESTVRYLAAEMAHVG 178

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 VN ISAG I+TL+ GV G+ ++KE + R V +VG+TAA+L+S L+SGV G  
 Sbjct: 179 HVNGISAGAIKTLAVSGVSGYKDLIKESDSRTADGVGVTIDDVQTA AFLVSPASGVIG 238

Query: 244 ENIHVDSGFH 253

+ ++VD G H  
 Sbjct: 239 DIVYVDKGVH 248

[>gi|27375882|ref|NP\_767411.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizoma japonicum]  
gi|27349020|dbj|BAC46036.1| NADH-enoyl acyl carrier protein reductase [Bradyrhizoma japonicum]  
 Length = 265

Score = 201 bits (512), Expect = 7e-51  
 Identities = 114/252 (45%), Positives = 158/252 (62%), Gaps = 2/252 (0%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLQAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 ++ K +IMGIAN SIA+G+AK L GA+L FT+ QL +  
 Sbjct: 5 MKGKRGGLIMGIANDHSIAWGMAKTLHAHGAELAFTFQGEALGKRVKPLAEQLGV--ELVL 62

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSETSREGFLLAQDISSY 123  
 DV+ V F+ + + G +D V H+I FA+ +L+GR+++TSRE F IS +  
 Sbjct: 63 PCDVEDIASVDAFDVLRKGKDFVIHAIGFADKNEALKGRYADTSRENFSRTMVISCF 122

Query: 124 SLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 183  
 S T VA A +LM EGGS++ T+ E A+ NYNVMGVAKA+LEA+V+YLA D GP I  
 Sbjct: 123 SFTEVAKRAAELEMTEGGSMITLTFGASERAMPNYNVMGVAKAALEASVRYLASDFGPRGI 182

Query: 184 RVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVTG 243  
 RVNA+SAGPIRTL+ G+G + +++ +PL+R V E+G +A YLLSDLGVTG  
 Sbjct: 183 RVNAVSAGPIRTLAGSGIGEARAMFAFMQKHSPLRRGVTLDELGGSALYLLSDLGSSGVTG 242

Query: 244 ENIHVDSGFHAI 255  
 E +VDSG++ +  
 Sbjct: 243 EIHYVDSGYNIV 254

[>gi|22975990|gb|ZP\_00021907.1| hypothetical protein [Ralstonia metallidurans]  
 Length = 260

Score = 201 bits (512), Expect = 7e-51  
 Identities = 113/253 (44%), Positives = 156/253 (61%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLQAKLVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K +I G+ + RSIA+G+A + GA+L FTY + +Y  
 Sbjct: 4 LAGKRILITGLLSNRSIAYGIAACKREGAELAFTYVGERFKDRITDFAKEFGSD--MIY 61

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 + DV SDE++ F +G+ DG+ HSI FA E + G F + SREGF +A DIS+  
 Sbjct: 62 ECDVGSDEQIDATFAALGQRWEKFDGLVHSIGFAPREAIAGNFLDGLSREGFRIAHDISA 121

Query: 123 YSLTIVAHEAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDI 182  
 YS +A A L+ + S++ TYLG E V NYN MG+AKASLEA+V+YLA +GP  
 Sbjct: 122 YSFPAKAAAMPLNDKASLLTLYGAERVVPNYNTMGLAKASLEASVRYLASAVGPRG 181

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 +R N ISAGPI+TL+A G+ F+ +LK E+ AP++RNV EVG AA+LLSDL+SGVT  
 Sbjct: 182 MRANGISAGPIKTLAASGIKDFSRLLKHFEDVAPIRRNVTIEEVGNVAAFLSDLASGVT 241

Query: 243 GENIHVDSGFHAI 255

GE +VD G++ +  
 Sbjct: 242 GEITYVDGGYNIV 254

[!]>gi|22982236|ref|ZP\_00027522.1| hypothetical protein [Burkholderia fungorum]  
 Length = 274

Score = 201 bits (512), Expect = 7e-51  
 Identities = 110/253 (43%), Positives = 158/253 (62%), Gaps = 3/253 (1%)

Query: 4 LENKTYVIMGIANKRSIAFGVAKVLDQLGAKLKVFTYXXXXXXXXXXXXQLNQPEAHLY 63  
 L K ++ G+ + RSIA+G+A+ + GA+L FTY + ++  
 Sbjct: 15 LAGKRILLTGLLSNRSIAYGIAQACRREGAELAFTYVGERFKDRIKEFAGEFGSD--LVF 72

Query: 64 QIDVQSDEEVINGFEQIGKDVGNIIDGVYHSIAFANMEDLRGRFSE-TSREGFLLAQDISS 122  
 DV D ++ F + + +DG+ HSI FA E + G F + +RE F +A DIS+  
 Sbjct: 73 PCDVADDAQIDALFASLQHWDGLDGLVHSIGFAPREAIAGDFLDGMTRENFRIAHDISA 132

Query: 123 YSLTIVAHAKKLMPEGGSIVATTYLGGEFAVQNYNVMGVAKASLEANVKYLALDLGPDN 182  
 YS +A A+ + S++ +YLG E A+ NYN MG+AKASLEA+V+YLA+ LG  
 Sbjct: 133 YSFPAKAAQSMFTPDaslltSYLGAERAIPNYNTMGLAKASLEASVRYLAVSLGAKG 192

Query: 183 IRVNAISAGPIRTLSAKGVGGFNTILKEIEERAPLKRNVQVEVGKTAAYLLSDLSSGVT 242  
 +RVN ISAGPIRTL+A G+ GF IL+ +E+ APL+RNV +VG TAA+LLSDL++GVT  
 Sbjct: 193 VRVNGISAGPIRTLAAAGIKGFGKILEFVEQNAPLRRNVTIEQVGNTAAFLSDLAAAGVT 252

Query: 243 GENIHVDSGFHAI 255  
 E +HVDSGF+A+  
 Sbjct: 253 AEIVHVDSGFNAV 265

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Mar 26, 2003 11:48 PM  
 Number of letters in database: 445,599,717  
 Number of sequences in database: 1,384,147

Lambda K H  
 0.316 0.135 0.368

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 190,169,730  
 Number of Sequences: 1384147  
 Number of extensions: 7112778  
 Number of successful extensions: 21006  
 Number of sequences better than 10.0: 1996

Number of HSP's better than 10.0 without gapping: 777  
Number of HSP's successfully gapped in prelim test: 1219  
Number of HSP's that attempted gapping in prelim test: 19003  
Number of HSP's gapped (non-prelim): 2046  
length of query: 256  
length of database: 445,599,717  
effective HSP length: 121  
effective length of query: 135  
effective length of database: 278,117,930  
effective search space: 37545920550  
effective search space used: 37545920550  
T: 11  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.6 bits)  
S2: 71 (32.0 bits)